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MIN; 63060;	PFAM; PF00498; FRA; 1.	MECHANOCHEMICAL (MOOR) (BY SIMILARITY).
PFAM; PF00495; FRA; 1.	PRINTS; PRO310; KINESIN-HEAVY.	COILED COIL (POTENTIAL).
PRINTS; PRO310; KINESIN-HEAVY.	PROSITE; PS00411; KINESIN MOTOR DOMAIN; 1.	COILED COIL (POTENTIAL).
Motor Protein; Microtubules; ATP-binding; Colled coil;	Motor Protein; Microtubules; ATP-binding; Colled coil;	COILED COIL (POTENTIAL).
Phosphorylation.	SEQUENCE 1103 AA: 123071 MW: F14C398DAB2C10 CRC64:;	ATP (POTENTIAL).
DOMAIN 1 355	Query Match 37 88; Score 2051; DB 1; Length 1103;	MECHANOCHEMICAL (MOOR) (BY SIMILARITY).
DOMAIN 1 355	Best Local Similarity 54 38; Pred. 0.00+00;	COILED COIL (POTENTIAL).
DOMAIN 1 355	Matches 340; Conservative 127; Mismatches 117; Indels 42; Gaps 28;	COILED COIL (POTENTIAL).
DOMAIN 1 355	1 MAGAS-VKAYAVRPFENARETSODAKVYSMGNQNTSINP-----K-Q-S-K---DAPK 48	COILED COIL (POTENTIAL).
DOMAIN 1 355	1 MSGCFQKVVYVRFENARETDQAGCIVRPMGNGNQTLIIPGGGEAKRARKSQTIDMPK 60	COILED COIL (POTENTIAL).
DOMAIN 1 355	49 SFTFEDYWSKTSITDPOFASQOQYRDIIGEMLHAFEGYNVNCIYAGTQAGKSYTM 108	COILED COIL (POTENTIAL).
DOMAIN 1 355	61 AFREDFRSWS-DRKNAQYAROEDLFDQGFLYDQMLNAKQGYNNCIYAGTQAGKSYTM 119	COILED COIL (POTENTIAL).
DOMAIN 1 355	109 1GROEQQVTFQDQEDLSFVNSVSAQ-1	COILED COIL (POTENTIAL).
DOMAIN 1 355	110 AFREDFRSWS-DRKNAQYAROEDLFDQGFLYDQMLNAKQGYNNCIYAGTQAGKSYTM 167	COILED COIL (POTENTIAL).
DOMAIN 1 355	120 G-YKG-ERHVPICODMRINLDRKNDKLCIVTBYSLIYERVDRDNLNSTGIVKT 177	COILED COIL (POTENTIAL).
DOMAIN 1 355	168 VRHPLIGQYDLSKLAVTSYADIAIDLDCNKRKARTAATNMENSSRSHAVFTVQ 227	COILED COIL (POTENTIAL).
DOMAIN 1 355	178 VREHPSTGQYDLSKLAVTSYADIAIDLDCNKRKARTAATNMENSSRSHAVFTVQ 237	COILED COIL (POTENTIAL).

FT	DOMAIN	425	445	COILED COIL (POTENTIAL).
FT	DOMAIN	598	632	COILED COIL (POTENTIAL).
FT	DOMAIN	777	797	COILED COIL (POTENTIAL).
FT	DOMAIN	183	335	MICROTUBULE-BINDING.
FT	DOMAIN	1460	1586	PH.
FT	DOMAIN	957	1052	ARG/LYS-RICH (BASIC).
FT	DOMAIN	1203	1584	ARG/LYS-RICH (BASIC).
FT	NP_BIND	93	100	AMP.
FT	VARIANT	598	598	Y > T.
FT	VARIANT	330	930	Y > W.
SEQUENCE	1384 AA.	1:79736 MW:	559462B3D29843 CRC64:	
Score	1975;	DB 1;	Length	1584;
Best Local Similarity	52.6%			
Matches	318;	Conservative	123;	Mismatches 12;
Indels	38;	Gaps	20;	
Query Match	36.4%			
Db	2	SSYKVAVRVRPFNRBISNTKCYLQYNGNTTIN--G--HSINKE-N-F----SFNF 49		
Oy	5	GNIKVVVRPWRNARIDGAKCIVKVRMENOTIUPPGAEKARKSGKTMDGKAF 64		
Db	50	DHSYWSAFRDPHPIRTOKQVVELGWMLLEHAFEGYVNCVLPAYGOTSGSKSYTHMGKAND 109		
Oy	65	DRSYASPKNAKPNYAKQDPLDQGIPDYLDAEKGYNCVLPAYGOTSGSKSYSMAG--YG 122		
Db	110	PDEGTYIPRLNLPLFARIDN-NNKDQISITVSTKTCVCEKVRDNLNSGSKYKREH 168		
Oy	123	KEH-GVTRICQDFRKRINLQDKRUDTCVVESTLNEVRDNLNSPGNLYKREH 181		
Db	169	PLLGYPDOLTRKAVESYDHICNDLNGKARTVATNNNETSSHISVHAPTFTVTKRHC 228		
Oy	182	PSTGYPVEDLAKLVRSFOTENLMDGNGKARTVATNNNETSSHISVHAPTFTQWKHD 241		
Db	229	ADSNLDETEKHKISLVDLAYERGKARTVATNNNETSSHISVHAPTFTQWKHD 288		
Oy	242	EETKMPTEKVKATSLVDLAYERGKARTVATNNNETSSHISVHAPTFTQWKHD 301		
Db	289	KKSNKGKVPYPRDVSITLLENUNGSNTAMLAISPDADINPDTSTYRADRQIV 348		
Oy	302	KOKKNO-LVPPRSVLTWLARDLSGSGNTAMLAISPDADINPDTSTYRADSRK 360		
Db	349	QAVWNEDEPAKTLRLENSEVTKRHLKDG---IDVTD--VQET--PKK--HKK-G 396		
Oy	361	NHAYVNEDENMARIMRLKELAQRSLLOSSCGGGGAGSGGPVPESTYPPDPLRQIV 420		
Db	397	P-KLP-AHVH--EGL-EKLOQESKLMIAEIGTKWMLKLIHETKREERLGMGLC 449		
Oy	421	SIQOPATVYKMSKATIVQNOKEKYLTDNOMEWKAKTEHHERAALPELGTS- 479		
Db	450	AEGTGTAVESPKPLPHLYNLDNPLMSCLLYYLKGNTSVGRPEAEHHPDILSCEAI 509		
Oy	480	IEKGFI-VGPYKISREPHLYNLDNPLMSCLLYYLKGNTSVGRPEAEHHPDILSCEAI 538		
Db	510	LEHRCFNEGGTYNTLTKPNASYCQVQITVPLHGSVILGEHHVNPQBAR 569		
Oy	529	LKHCFTFENVWVNTIPVNEKAQWVNGVRLDKTFLRSCYRITGDFHFNHPEBAR 598		
Db	570	QSRHN 574		
Oy	599	AERQE 603		
RESULT	6	STAPU	STANDARD;	PRT: 639 AA.
ID	K122	STAPU	STANDARD;	PRT: 639 AA.
AC	P16877			
DT	01-Nov-1995 (Rel. 32, Created)			
DT	01-Nov-1995 (Rel. 32, Last sequence update)			
DT	15-Dec-1996 (Rel. 37, Last annotation update)			
GN	KINESIN-II 85 kDa SUBUNIT (KRP-85/95 85 kDa SUBUNIT).			
OS	Strongylocentrotus purpuratus (Purple sea urchin).			
OC	Eukaryota; Metazoa; Echinodermata; Echinocozoo; Echinolidea;			
OC	Echinoloidae; Echinacea; Echinoida; Strongylocentrotidae;			
OC	Strongylocentrotus.			

RN	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RP	RP
TC	ISSUE=66;
RX	MEDLINE: 940500179.
RA	Colle, D. G.; Chinn, S. W.; Wedaman, K. P.; Hall, K.; Vuong, T.,
RA	Scholey, T. M.;
RA	*Novel heterotrimeric kinesin-related protein purified from sea urchin eggs.;
RT	Nature 366:268-270 (1993).
RL	CC-1 SUBUNIT: TRIMER OF A 115 kDa SUBUNIT AND TWO KINESIN-LIKE SUBUNITS
CC	OF 95 AND 85 kDa.
CC	1- PTM: THE N-TERMINUS IS BLOCKED.
CC	1- SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY. KINESIN II SUBFAMILY.
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.ebi-sib.ch/announce/).
CC	DR: L16993; RAA16989; 1.;
DR	DR PFM; P00225; kinesin; 1;
DR	DR PRINTER; P00380; KINESIN; MOTOR_DOMAIN; 1;
DR	DR PROSITE; PS00411; KINESIN; MOTOR_DOMAIN; 1;
DR	DR PROSITE; PS50067; KINESIN; MOTOR_DOMAIN; 1;
KW	Motor protein; Microtubules; ATP-binding; Coiled coil; MACHINOCHEMICAL (MOTOR); BY SIMILARITY.
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FT	FT DOMAIN 2 620
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175	PDGVYIKDLISAYVNNAIDMDRIMTIGKHNSGATHNNEHSSRAHTITIECSERG	234	Db	5	SAETVTKVVRCPNNKISQGKHKIVEMDKRG -KVEVTPN -KGP -PGEP - N - KSF 56
182	PTGVEYDVKLAVYRVSQFPEIENLDEKARTVYATNNNTTSRRHAYFLUTLUTORMHD	241	Qy	3	GGGNKTKVVRVPFIAEBOGAKAVITVEMGNOTLTPPAAKEKARSGTMDKPF 62
235	IDGNMHDY -RNGKHLVYDLAGSERQAKTAGCQKTKINLSESLGHNVIALVD -G	290	Db	57	TEVDYDWN -SKOIDY --DEFERSL -V --DSVLOGNFTIYAGTQGKTFKTMEGV 108
242	ETKIDKPKYKATSYDULASBPAVSTAGATKKGATITRSLGNSVAAALAMSSC	301	Qy	63	ADPSY -WEDNANVYAPRQDQDGYVLLNARKGKNCFAYGQSKCMEY 121
291	K - 5TH -VPRISKTRLQDLSIGGNTSTACANICPADVDTSTLVRANAKTIN	347	Db	109	RSPNPLGCVPSNFHFTIARTQONQFL - -VRSLEYKETROLAKOKRKLDSL 165
302	KOKKHPOLVYDROSVLWILADSUGGSNTMANTASPADINFESTLURFADSAKINN	361	Qy	122	-OK -E -RGPVRCODNFREINLORDKNUCTEVSTLERYNRVDRPLPSTKGNLAV 178
348	KARINEPDALLAROFELREJEDL -GEEISDOSIDSEEDDECEGEVGDGKRK	406	Db	166	KERPDGVYKOLSSFTVSKVSKVHATVHVNNSVSTOMHRSERSHALFITECS 225
362	HAVNEDPARNMIRLEKELAQRSKLOSSGGGAGGGPVESYSPDPLPQIVS	421	Qy	179	REHPSTGPYEDLAVYRVSQFQINLDESNFARTVATMNTTSRSHAVFTLTQD 238
407	KRTIGKSKVSPDRME -M -Q -KIDE -RKALMGEPEERKARALE 455	421	Db	226	ELGPQDGH1 -RVGKLAVLVLQASRQATGDFDEKATKINLSSALGVNSVALD - 283
422	IQOPDVKYKMSKATIQUEQNSKLYRDUNQNWEEKLAKTEELHREADE 474	421	Qy	239	WHDEBTERMCTEKYANISYDLSLAGERSATSTGAGLKEAINEBSLGLRVTANADM 298
			Db	284	--GK - -SSH - IGYRDUKTLPLQDSGGNATKMTLQDLSUGNSNTMIAISPDINFEELSLTRPADSKR 338
			Qy	299	SSGQKQKNNQVPPRQSTLMLLDSUGNSNTMIAISPDINFEELSLTRPADSKR 358
			Db	339	IKNNPKKNEIDPDLARFPEEISRLQALKGKPSDG 376
			Db	341	DT - 01 -NOV-1995 (Rel. 32, Created)
			Db	342	DT - 01 -NOV-1995 (Rel. 32, Last sequence update)
			Qy	359	IKRNHAYVNEDPNARMLKEELAQLRSKLOSSGGGG 396
			Db	390	DT - 01 -OCT-1996 (Rel. 34, Last annotation update)
			Db	391	DT - 01 -OCT-1996 (Rel. 34, Last annotation update)
			Db	392	KINN - LIKE PROTEIN K39 (FRAGMENT).
			Db	393	KINN
			Db	394	OS - Laishmania chagasi
			Db	395	OC - Kinetoplastida: Trypanosomatidae; Leishmanias.
			Db	396	OC - Euglenozoa;
			Db	397	RN - Kinetoplastida: Trypanosomatidae; Leishmanias.
			Db	398	RN -
			Db	399	RP -
			Db	400	ID - KIN1_LICH STANDARD; PRTP;
			Db	401	PRTP;
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DR EMBL: AB002357; BAA0815; 1;
DR HSSP: P06536; 2; KIN.
DR MM: 603754; -.
DR PPM: P00235; 1; kinesin; 1;
DR PRINS: PRO0380; KINESINHAWV.
DR PROSIT: PS00340; KINESIN; MOTOR-DOMAIN; 1.
DR Motor protein; Microtubules; ATP-binding; Coiled coil; Neurone.
RW DOMAIN; 1; 345; MECHANOCHEMICAL (MOTOR) (BY SIMILARITY).
DR DOMAIN; 1; 346; 579; COILED COIL (BY SIMILARITY).
FT DOMAIN; 1; 96; 103; GLOBULAR.
FT NP_BIND; 1; 393; ATP (POTENTIAL).
FT DOMAIN; 1; 396; 406; POLY-GLY.
FT DOMAIN; 1; 723; 730; POLY-GLU.
FT SQ SEQUENCE; 747 AA; 85125 MW; 97FAA573AFA87023 CIRG64;
Query Match Similarity 17.4%; Score 945; DB 1; Length 747;
Best Local Similarity 47.0%; Pred. No. 4; 7.8e-160;
Matches 164; Conservative 72; Mismatches 99; Indels 14; Gaps 9;
Db 37 KLGIVSYVKPKTAEMPKPTFDVDAWNAQKELDYLDETRPLVDSVLQENGTIPAYG 96
QY 50 KSGRTIMDQPKAFADRS-YWSKDNAPNTAPRQDQFLDQGVPILNAPKGTYNCIIFYG 108
Db 97 QTGTQTYMEIGRIGDPEKRGVTPNSPDHLFTHLTSRQNSQVYL - VRASTLYQEBR 153
QY 109 QTGSGSYSMGMY-GK-E-HGTVTRICODMRINELQDKNUTCIVVEYSLYIENVR 165
Db 154 DLISKQOTKRLKEPKRPTGIVYDLSSTFTVSKWKELEYAWNGNQNSVGATNNNESS 213
Qy 166 DLINNPSTKRNLYKRENPSSGPVYDPLBKLQVRSQTEENIDEGNARVTAATNNNESS 225
Db 214 RSHAIKVITI-ECSEVGLDGENHHRVGRKLNUVLDLAGEERQAKTGAQERLKEATKINSL 272
Qy 226 RSHAVPFTLQKWHDEETKNDTEKVKASIVDLSSEERATSTGATGARLKEAGINSL 285
Db 273 SALGNTISALD -- GK -- SHH -- PPKDSDGKAKTIVWANGPASVNE 326
Qy 286 STGVRVIAADMSCKSKKQHQLPVDSSWTLKDSLGSNSMTMIAISPADINPEE 345
Db 327 TLFTRYAARAKNPKNPRVNDLREFQETARLKAQLEKRSIG 375
Qy 346 TLSTLRYAASRINHAWVNDENPARNMIRELKEAQLRSKIQSSGG 394
RESULT 12
ID KFP2_MOUSE STANDARD; PRN; 747 AA.
ID 061771; 36. Created)
DT 15-JUL-1998 (Rel. 36. Last annotation update)
DT 15-JUL-1998 (Rel. 36. Last annotation update)
DE KINESIN-LIKE PROTEIN KIF3B (MICROTUBULE PLUS END-DIRECTED KINESIN MOTOR 3B).
GN KIF3B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Mus.
OC (1)
RN SP00124.
RP SOURCE FROM N.A.
SPRATN-ICR; TISSUE-BRAIN;
RC MEDLINE; 96032268.
RA Tamazaki H.; Noda T.; Ohada Y.; Hirokawa N.;
RT KIF3B: a heterodimeric kinesin superfamily protein that works as a microtubule plus end-directed motor for membrane organelle transport.;
RL J. Cell. Biol. 130:1387-1399 (1995).
CC FUNCTION: MICROTUBULE-BASED ANTEROGRADE TRANSLOCATOR FOR MEMBRANOUS ORGANELLES. PLUS END-DIRECTED MICROTUBULE SLIDING

CC ACTIVITY IN VITRO.
 CC -1: SUBUNIT: HETERO-DIMER OF KIF3A AND KIF3B.
 CC -1: SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY. KINESIN
 CC -1: SUBFAMILY: .

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 CC or send an email to license@isb-sib.ch).
 DR D26077; BRA05070.1; -.
 DR HSSP; P65356; 2KIN.
 DR PFAM; PF00225; Kinesin; 1.
 DR PRINS; PR00380; KINESIN_HUMAN.
 DR PROSTE; PS00411; KINESIN_MOTOR_DOMAIN; 1.
 DR PROSTE; PS50067; KINESIN_MOTOR_DOMAIN; 1.
 KW Motor protein; Microtubules; ATP-binding; Coiled coil; Neurone.
 PT DOMAIN 1 345 MECHANOCHEMICAL (MOTOR) (BY SIMILARITY).
 PT DOMAIN 346 579 COILED COIL (BY SIMILARITY).
 PT DOMAIN 580 747 GLOBULAR.
 PT DOMAIN 96 103 ATP (POTENTIAL).
 PT DOMAIN 386 393 POLY-GLY.
 PT DOMAIN 394 405 POLY-GLU.
 PT DOMAIN 723 730 POLY-SER.
 SO SEQUENCE 747 AA: 85288 MR: FAJ36A4190ECBB47 CRC64;

Query Match Score 942; DB 1; Length 747;
 Best Local Similarity 17.4%; Score 942; DB 1; Length 747;
 Matches 163; Conservative 73; Mismatches 99; Indels 14; Gaps 9;

Db 37 KLGQSVNPKGSHEMKRTTDAYDNNAKOPELYDTERPLVDSVQGNGNTIAYG 96.
 Qy 50 KSKTKTMQPAFORS-YWSDKQKAPYQARQDIFQDGLPQDIAFNGKGNQFCIAYG 108
 Db 97 QTGTGTTMGRGDPKPERKVPINSPDHTTHISHSQHQQL--VRASTLEYOBIR 153
 Qy 109 QTSGRSKSMGTYGR-B-HEVTPRCQMPFRNQLQDNKLCITVEYIYERV 165
 Db 154 DLISDKTQKLEKKEPDRGTYQYKDLSEFTVKSYKEIHWYNGNQNSYGTANNHEHSS 213
 Qy 166 DLNPSTPNKUWKRNPSTQVEDAUYRSPQELNMDENSKARTVATRNNETSS 225
 Db 214 RSHAFVUTI-ESESEWLGDSNH1PRGKLNWYDQSEPAQTAQCEELKAPKINSL 272
 Qy 226 RSHAFVUTI-LQWHDEETKADTEKAKLSDAERATSTGATGARLGKAGINRSL 285
 Db 273 SALGVNISALVD---GK---STH---IPROSOKTRLQDLSGJNRAVYANVSPASYNVE 326
 Qy 286 STGVRVIAALADSSKORKNQKLYPDSWVNLKDSLGSNMTANIAISPADINFE 345
 Db 327 TUTLTYANRAKIKURKVERPDQKLAERFQETARKAQLKEKRG 375
 Qy 346 TSLTRYADSAKIKHAYVNEDNARMIRELKELAQLRNLSSCGG 394

RESULT 13
 ID K168 DROME STANDARD; PRT: 784 AA.
 AC P45857; 1
 DT 01-NOV-1995 Rel. 32 (Created)
 DT 15-JUL-1996 (Rel. 32, Last sequence update)
 DE KINESIN-LIKE PROTEIN KIF6B.
 GN KIF6B or KIF5.
 OS Drosophila melanogaster (fruit fly).
 OC Pieridae; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Phrygidae; Drosophilidae; Drosophila.
 RN [1]
 RP SEQUENCE FROM N. A.

RX MEDLINE: 95050960.
 RA Stewart R.J.; Goldstein L.S.B.;
 RA Pesavento P.A.; Woerpel D.N.; Goldstein L.S.B.;
 RT "Characterization of the KIF6B0 Kinesin-like protein in Drosophila:
 RT possible roles in axonal transport.";
 RT J Cell Biol. 127:1041-1048 (1994).
 RN [2]
 RP SOURCE OF 220-342 FROM N.A.
 RX Stewart R.J.; Pesavento P.A.; Woerpel D.N.; Goldstein L.S.B.;
 RA Kinesin superfamily in Drosophila.
 RT Proc. Natl. Acad. Sci. U.S.A. 88:8470-8474 (1991).
 CC -1: FUNCTION: PLUS-END DIRECTED MICROTUBULE MOTOR THAT MAY BE USED FOR
 CC ANTERGRADE AXIAL TRANSPORT AND COULD CONCEIVABLY MOVE CARGOES IN
 CC FLY NEURONS DIFFERENT FROM THOSE MOVED BY KINESIN HEAVY CHAIN OR
 CC OTHER PLUS-END DIRECTED MOTORS.
 CC -1: TISSUE SPECIFICITY: EXPRESSED PRIMARILY IN THE CENTRAL NERVOUS
 CC SYSTEM AND IN A SUBSET OF THE PERIPHERAL NERVOUS SYSTEM DURING
 CC EMBRYOGENESIS.
 CC -1: SIMILARITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY. KINESIN
 CC II SUBFAMILY.
 CC ---
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 CC SYSTEM AND IN A SUBSET OF THE PERIPHERAL NERVOUS SYSTEM DURING
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 CC ---
 DR PDB: U15674; MAA65929; 1; -.
 DR PDB: U74431; MAA28558; 1; -.
 DR HSSP: P56326; 2KIN.
 DR PROTEIN: PS00044; 181; K1p68D.
 DR PFBASE: PFB300044; 1.
 DR PFAM: PF00225; 1.
 DR PROSITE: PS0380; 1; KINESIN_HUMAN.
 DR PROSITE: PS5067; KINESIN_MOTOR_DOMAIN1; 1.
 KW Motor protein; Microtubules; ATP-binding; Coiled coil.
 FT DOMAIN 16 275 MECHANOCHEMICAL (MOTOR).
 FT DOMAIN 351 385 COILED COIL (POTENTIAL).
 FT DOMAIN 426 582 COILED COIL (POTENTIAL).
 FT NP_BIND 106 113 ATP (POTENTIAL).
 FT CONFLICT 220 221 SS > TC (IN REF. 2).
 FT GSRK -> VRGQV (IN REF. 2).
 SQ SEQUENCE 784 AA: 88193 MW: 949BBB0D072FEC0 CRC64;
 DR PDB: U15674; MAA65929; 1; -.
 DR HSSP: P56326; 2KIN.
 DR PROTEIN: PS00044; 181; K1p68D.
 DR PFBASE: PFB300044; 1.
 DR PFAM: PF00225; 1.
 DR PROSITE: PS0380; 1; KINESIN_HUMAN.
 DR PROSITE: PS5067; KINESIN_MOTOR_DOMAIN2; 1.
 KW Motor protein; Microtubules; ATP-binding; Coiled coil.
 FT DOMAIN 16 275 MECHANOCHEMICAL (MOTOR).
 FT DOMAIN 351 385 COILED COIL (POTENTIAL).
 FT DOMAIN 426 582 COILED COIL (POTENTIAL).
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 DR PROSITE: PS5067; KINESIN_MOTOR_DOMAIN2; 1.
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 DR PROSITE: PS5067; KINESIN_MOTOR_DOMAIN2; 1.
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 FT DOMAIN 426 582 COILED COIL (POTENTIAL).
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 FT NP_BIND 106 113 ATP (POTENTIAL).
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 DR PDB: U15674; MAA65929; 1; -.
 DR HSSP: P56326; 2KIN.
 DR PROTEIN: PS00044; 181; K1p68D.
 DR PFBASE: PFB300044; 1.
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 DR PROSITE: PS0380; 1; KINESIN_HUMAN.
 DR PROSITE: PS5067; KINESIN_MOTOR_DOMAIN1; 1.
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 FT DOMAIN 426 582 COILED COIL (POTENTIAL).
 FT NP_BIND 106 113 ATP (POTENTIAL).
 FT CONFLICT 220 221 SS > TC (IN REF. 2).
 FT GSRK -> VRGQV (IN REF. 2).
 SQ SEQUENCE 784 AA: 88193 MW: 949BBB0D072FEC0 CRC64;
 DR PDB: U15674; MAA65929; 1; -.
 DR HSSP: P56326; 2KIN.
 DR PROTEIN: PS00044; 181; K1p68D.
 DR PFBASE: PFB300044; 1.
 DR PFAM: PF00225; 1.
 DR PROSITE: PS0380; 1; KINESIN_HUMAN.
 DR PROSITE: PS5067; KINESIN_MOTOR_DOMAIN2; 1.
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 DR PROTEIN:

Query Match 15.6%; Score 846; DB 1; Length 1231;
 Best Local Similarity 47.8%; Pred. No. 1.71e-139;
 Matches 163; Conserv. 70; Mismatches 82; Indels 26; Gaps 18;

Db 46 DKSF-TYDFYFDPS-TEQEDEVNTAVAPLJKGVKGNNATVLAGQGSGCKTYSNCGGAYT 103
 Qy 65 DRSYKFD-KNAPNAYARQEDLFODLGVPLDNRKGNMCTFAGGNGCSKSYMMG-Y 121

Db 104 AEGBHSAAGTGTGTRVYQLEKEIN- KKS- DEFTLVKYLINNELLDCSSREKAT 160
 Qy 122 G-KEH---GTVRICOQDFRINNEQDKNUCTIVESTLTVRROLL-NFSTKGN 175

Db 161 QINIRDPRKESGKIVGLTGTKVLYASDPTVSCL-EGQRNBTVASTANNSOSSRSASHAETI 219
 Qy 176 -LKVREHHSSTOPVYEDLA-KLVVSKQETENIMDEGKARTVATNNNETSRSASHAFTL 233

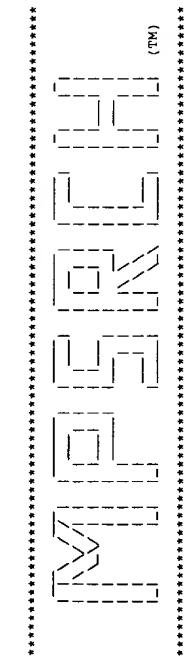
Db 220 SIEQR-KIND-KNSFR-SKHLVLDLAGSERQTKAEGDRLLRGINTNFGSLCHGNVIS 276
 Qy 234 TLTKQKHDEETKDKTDEKVKASLVDLAGERATSRGATGARKEGAEINFSSTUGRIA 293

Db 277 ALGD---DKKGNEPYDSEK-TRALQDGSCHSHPLMACYSEPSNULFETLSTLRYA 331
 Qy 294 ALADMSGKQKQKQLYPDSYSLTWLKKLOGNSMTAMIAISPADINFEETLSTLRYA 353

Db 332 DARKTKNPKTINIDPOQAELNHJKQVOQDQJLQAG 372
 Qy 354 DSARIKIHAVNEDPNAMIRLEKELLAQURSKL-OSSEG 393

Search completed: Mon Aug 21 15:40:50 2000
 Job time : 30 secs.

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21	791	14.6	2954 13	042263	KINESIN-RELATED PROTEIN	9.32e-130
22	777	14.3	968 3	P8199	KINESIN MOTOR PROTEIN	7.47e-127
23	776	12.2	5	Q92229	HYPOTHETICAL 13.5-8 KD	7.47e-127
24	716	13.6	1388 13	Q97785	KLP2 PROTEIN	2.28e-118
25	714	13.5	150 4	Q95068	MICROTUBULE-BASED MOTO	5.89e-118
26	732	13.5	1254 5	K74663	K7 KINESIN-LIKE PROTEIN	1.53e-117
27	720	13.3	814 5	B93945	KINESIN-LIKE PROTEIN	4.55e-115
28	704	13.0	197 11	B98857	KINESIN-LIKE PROTEIN	9.10e-112
29	703	13.0	1027 11	Q92279	KINESIN HEAVY CHAIN	1.45e-111
30	697	12.9	151 3	Q91112	KINESIN HEAVY CHAIN FK	2.48e-110
31	701	12.9	784 3	Q59751	POTENTIAL KINESIN-LIKE	3.73e-111
32	696	12.8	160 11	Q35063	MOTOR DOMAIN OF KIF13A	3.98e-110
33	695	12.8	160 11	Q35062	MOTOR DOMAIN OF KIF13A	6.40e-110
34	696	12.8	956 11	P02828	KINESIN HEAVY CHAIN	3.98e-110
35	696	12.8	1083 5	Q4935	KIAA0511 PROTEIN	2.65e-109
36	688	12.7	151 13	Q91116	KINESIN HEAVY CHAIN FK	1.10e-108
37	688	12.7	1130 5	P02633	P02632 PROTEIN	3.00e-107
38	689	12.7	987 10	Q81635	KINESIN-LIKE HEAVY CHA	8.20e-106
39	682	12.6	1014 11	Q92110	KINESIN-RELATED MITOTI	1.03e-101
40	675	12.4	773 13	P77980	MICROTUBULE-BASED MOTO	6.41e-102
41	676	12.4	1200 5	P92277	PPCB66W PROTEIN	2.77e-100
42	654	12.0	687 4	Q73399	MICROTUBULE-BASED MOTO	6.76e-100
43	651	12.0	1893 5	Q17887	TGFL1 PROTEIN	6.76e-101
44	626	11.5	932 5	Q17753	SIMILAR TO KINESIN-LIK	8.61e-96
45	626	11.5	932 5	Q17753	SIMILAR TO KINESIN-LIK	8.61e-96

ALIGNMENTS

RESULT	1	PRELIMINARY;	PRT;	1770 AA.
ID	Q02119			
AC	Q02119			
DT	01-MAY-1999 (TPIBML1, 10, Created)			
DT	01-MAY-1999 (TPIBML1, 10, Last sequence update)			
DT	01-MAY-1999 (TPIBML1, 10, Last annotation update)			
DE	KIF1B-BEST.			
DN	KIF1B.			
OS	Mus musculus (mouse).			
OC	Bukarotia; Rodentia; Chordata; Vertebrata; Mammalia;			
RN	[1]			
RC	SPRAIN-ICR MOUSE.			
RA	NAKAGAWA T.; HIROKAWA N.;			
RT	*Identification and characterization of a new kinesin superfamily			
RT	Sequence from N.A.			
RP				
DR	SPRAYKERSHSPSPDPECESSORVYNDIGKEMIILAFEGNYNCIRAYCQGACKSYTM			
DR	Submitted (PDB:1999) to the PDB/GenBank/DBJ databases.			
DR	AB023556; BRA2523; 1.			
DR	PROSTIE; PS00411; KINESIN-MOTOR-DOMAIN; 1.			
KW	Motor protein; Microtubule-ATP-binding; Colled coll.			
SQ	SEQUENCE 1770 AA; 198851 MW; 4F52FC CRC32;			

Statistics: Mean 52.569; Variance 102.972; scale 0.51

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match Length	DB ID	Description	Pred. No.	Score 2215: 40.9%;
1	2215	40.9	1770 11	Q92119	KIF1B-BETA.	Pred. No. 0.0e+00;
2	2051	37.8	1103 4	Q75186	KINESIN-RELATED PROTEIN	0.0e+00
3	2006	37.0	1097 11	Q35787	KINESIN-RELATED PROTEIN	0.0e+00
4	1971	36.4	1384 5	Q18778	C_ELEGANS_UNC-104_KIN	0.0e+00
5	1858	34.3	1816 11	Q9W65	KIF1B MAJOR ISOPROM	0.0e+00
6	1849	34.1	689 11	Q8B58	KINESIN-LIKE PROTEIN K	0.0e+00
7	1597	29.5	1921 5	Q01349	KINESIN-73	1.31e-100
8	1308	24.1	1668 4	Q10558	KIF1A012 PROTEIN	9.45e-139
9	1291	23.9	928 5	Q9997	POTENTIAL KINESIN-LIKE	3.96e-135
10	1124	21.7	1516 5	Q2088	SIMILAR TO KIF1B; RBL	1.10e-199
11	958	17.7	702 4	Q19196	KINEIN FAMILY MEMBER	1.2e-164
12	904	16.7	744 13	Q39378	KINEIN-LIKE PROTEIN 3	2.51e-153
13	857	15.8	1121 5	Q18389	KINEIN-LIKE PROTEIN	1.71e-143
14	857	15.8	1121 5	Q02030	KINEIN-LIKE PROTEIN	1.71e-143
15	854	15.8	1121 5	Q16666	KINEIN-LIKE PROTEIN A	1.66e-143
16	850	15.7	1121 5	Q1890	CHROMATIN ASSOCIATED	4.9e-142
17	822	15.2	402 4	Q9Y4V4	(FRAGMENT).	3.3e-136
18	823	15.2	1225 13	Q09426	CHROMOKINESIN	2.0e-136
19	825	15.2	1226 13	Q91784	KINEIN-LIKE PROTEIN 1	7.9e-137
20	795	14.7	929 3	P78118	KINESIN.	8.54e-131

Db 168 VREHFLIGPVEDLEKLAFTYDADLMAGKRTAATNNNNNRSRSHAVTIVTQ 227

Db 161 AFADRSYTFEDK-NAPYKQRDGFQDLYPDLAERGKINGTCATGQSKTYSWMA 119

Db 109 GQFQSQAGTIPOLCELEFKIND-NCNEEMNISTSEVSKMELTCERVLRUNPKNGN 167

Db 120 GYKGE-HI-GYTRICQDMFRNLQKDNKUTQEVSYLTYINVRVRLNPKGNK 177

Db 178 VREHFSGPGVYDPLAKLYVRSCEENLDEGKNTKAATVNNNNNNSHAYPTUTQ 237

Db 228 KKRDPBNLSTEVKSKISLVDLGSERFADSTGKCTRLKEGANINNSLTUGKVISALE 287

DR	167	VREHPILGPVYDLSKLAVTSYADIADLDCNKAARTVATNMETSRSHAVFTVFTQ	226	PRINTS; PRO0380; KINESINHEAVY.
KW	178	VREHPSTPVEYLAKVRSQFQINLDEGNARTVATNMETSRSHAVFTVFTQ	237	Motor protein; Microtubules; ATP-binding; Coiled coil.
Qy	227	RSDIDOLSEKVISVNLVLAGRSRASSGCHRLKEGANIKSLTLLGKVISALAD	286	Score 1971; DB 5; Length 1584;
Db	238	KWIDDETMDETEKVANISVPLAGRASRATSGAYLAREGAEINRSLSTLRVTAALAD	297	Best Local Similarity 52.6%; Pred. No. 0/00e-00;
Qy	287	LGS-KKRSDFDIPYRDSVTLKLENUGGNSRTMTAAISPADINYBETSLRVAARTK	345	Matches 318; Conservative 122; Mismatches 127; Indels 38; Gaps 20;
Qy	298	MSGSGQKQKQVYVPRSVLTLVLLKDSIGNSNTMIAASPADINYBETSLRVAARTK	357	Db 2 SSYKAVNVRPVEPFIENSYNSKCVLQVNGNTTIN--G-HSINNE-N-F----SFNF 49
Db	346	QTCRHNVEDPARLIRLQEYALRLLMAGLSAALGGLKVKVEGSGPGVLPASS	405	Qy 5 GNIKVVPRFNAEIRLGKQVAVAGNOTILTPGAAEKAHSQGTIMDPRKAF 64
Qy	358	RKRNHVNVEDPARLIRLQEYALRLLMAGLSAALGGLKVKVEGSGPGVLPASS	409	Db 50 DWSYWSFARDNPHTKQVEYLGEMLETAEGTNCQGSKSSTHGKAND 109
Db	406	PPAPASPPSPPPHNGLPLSPSPSPSPAPQIGPPEAMERLQETKIAIPLNTHWERLKTE	465	Qy 65 DWSYWSFDPKAPYARQDOLPGLDNPAGKGNINCAYCQGSKSSTHGKAG--YG 122
Db	409	YP-PPDPLQKQVSIQ-OPD-A-TVK-KNRAEYVQQLQSKYRDLQWTEWERLKTE	463	Db 110 PDEMGILPRLNDPLARDIN-NIDKQVSYEVSNTYMEYTCRVQDNLQJNNSGNLVRH 168
Db	466	ALMFEREALAAENGSPGGWRYVGFSPKTPHLYNLDPEMLSCYLHYKQDVTYRGQV	525	Qy 123 KEH-CVPRICDPMFRINELQDKNLKCTVESYLTYNERYVIDLNSPKGKLYRKH 181
Qy	464	EINKERBEEALEEGTISIEKGKEMPHNLNSDPLAECIYNNKQTRIGNNV	523	Db 169 PLEGYDYLDTKMANCSDHICLMDENKNARTVATNMETSRSHAVFTVFTQ
Db	526	--D-V--DVKTGQFPTBNCUPLCPTISIOPDGEVATMELPQDPAEYVNCALVPELUVKSG	581	Db 288 PSTGYVYDYLAKLYVRSQFQEENLDEGENKARTVATNMETSRSHAVFTVFTQ
Qy	524	NQDTQAEERLNGSKILKERTCENV--D-NV-VTLPVHEKAVAVNGVDRKPTLRSQ	578	Db 229 ASNLDEPEKISKISLVDLASERANSTAEQOLKAGANIKNSLTIGVYKLAESTK
Db	562	NRVKGKHHVPRNHPPEAERLVE	605	Db 242 EETKADTEVAKISLVDIASERATGATLKGASINRSLTGIVRVAALAMISSC 301
Qy	579	YRITGDPHTRNHPPEAERLVE	602	Db 289 KKRKSQGVYVPPYDOSLTMUDRENGNSKTMALAAISPADINDEPLSLPLRYADRAKIV 348
Qy	302	KORKHQ-QVPPYDVSYTMLKJLSDGGSNSKMTATAISPADINBETLPLRYADSARRK	360	Qy 302 KORKHQ-QVPPYDVSYTMLKJLSDGGSNSKMTATAISPADINBETLPLRYADSARRK 360
Db	349	CAVNNEDPNAKJLRENEVFLRHLIKDG---IDVTD--VQBT--PQK--HKK-G 396		Db 349 CAVNNEDPNAKJLRENEVFLRHLIKDG---IDVTD--VQBT--PQK--HKK-G 396
Qy	361	NHAYVNEDPNAKJLRENEVFLRHLIKDG---IDVTD--VQBT--PQK--HKK-G 396		Qy 361 NHAYVNEDPNAKJLRENEVFLRHLIKDG---IDVTD--VQBT--PQK--HKK-G 396
Db	397	P-KLP-AHNV---BQL-EKUQSEKLMAEIGKWTQKDLQHTEFLRDLMCAC 449		Db 397 P-KLP-AHNV---BQL-EKUQSEKLMAEIGKWTQKDLQHTEFLRDLMCAC 449
Qy	421	STQDQDPTVAKKSKAEITQOLNSKELYRDNQWTEKLAKTETKNEKEAALBEGLS	479	Db 397 P-KLP-AHNV---BQL-EKUQSEKLMAEIGKWTQKDLQHTEFLRDLMCAC 449
Db	450	AEDGTCIGVSFSPKLPHVNLNDPENSECITYLVEGTYSVGRPAERPDILLSCEN	509	Qy 421 STQDQDPTVAKKSKAEITQOLNSKELYRDNQWTEKLAKTETKNEKEAALBEGLS 479
Qy	480	1EKG-VGPHTSRMPLHVNLSDPPLAECLVUNLNPOTRIVGNVNDQAEIRLANSKI 538		Db 450 AEDGTCIGVSFSPKLPHVNLNDPENSECITYLVEGTYSVGRPAERPDILLSCEN 509
Db	510	LELBHFEDNGDVTGFLTHKPNACSYNQVPTLMTGSRVBLGHVPRYDPOEAR 569		Qy 480 1EKG-VGPHTSRMPLHVNLSDPPLAECLVUNLNPOTRIVGNVNDQAEIRLANSKI 538
Qy	539	LKEHFTENDVNTVIVENKAAYVNVYRDPFLRSGRILDFDIFRHFNPHEAR 598		Db 510 LELBHFEDNGDVTGFLTHKPNACSYNQVPTLMTGSRVBLGHVPRYDPOEAR 569
Db	570	QSRHN 574		Qy 539 LKEHFTENDVNTVIVENKAAYVNVYRDPFLRSGRILDFDIFRHFNPHEAR 598
Qy	599	AERQE 603		Db 570 QSRHN 574
RESULT	5	PRELIMINARY;		Qy 599 AERQE 603
ID	QWHE5	PRELIMINARY;		Qy 539 LKEHFTENDVNTVIVENKAAYVNVYRDPFLRSGRILDFDIFRHFNPHEAR 598
AC	QWHE5	PRELIMINARY;		Db 570 QSRHN 574
DT	01-Nov-1995	(TREMBLrel. 12, Last sequence update)		Qy 599 AERQE 603
DT	01-Nov-1995	(TREMBLrel. 12, Last annotation update)		Qy 539 LKEHFTENDVNTVIVENKAAYVNVYRDPFLRSGRILDFDIFRHFNPHEAR 598
DE	C-LEGANS	UNC-104 KINESIN-LIKE PROTEIN (PIR:JN0114).		Db 570 QSRHN 574
CN	UNC-104			Qy 539 LKEHFTENDVNTVIVENKAAYVNVYRDPFLRSGRILDFDIFRHFNPHEAR 598
OS	Caenorhabditis elegans			Db 570 QSRHN 574
OC	Eukaryota; Metazoa; Nematoidea; Rhabditida; Caenorhabditis.			Qy 539 LKEHFTENDVNTVIVENKAAYVNVYRDPFLRSGRILDFDIFRHFNPHEAR 598
RN	[1]	SEQUENCE FROM N.A.		Qy 539 LKEHFTENDVNTVIVENKAAYVNVYRDPFLRSGRILDFDIFRHFNPHEAR 598
RX	WILSON R, ALNSCOUGH R, ANDERSON K, BAINES C, BEAKS M, COULSON A, COUSEY T, COOPER J, COULSON A., CRAXTON M, DEAR S, DU Z, DUBBIN R, FAVELL A, FULTON L, GARDNER A, GREEN P, HAWKINS T, HILLIER L, JONES M, KERSHAW J, LISTER J, LATREILLE P, LIGHTNING J, LLOYD C, MCMURRAY A, MORTIMORE B, O'CALLAGHAN M, PARSONS J, PERCY C, RIEKEN L, ROOPRA A, SAUNDERS D, SHIGGWEEKIN R., SMALDON N, SMITH A, SONNHAMER E, SPADEN R, SULLISTON J., THIERRY MIEG J, THOMAS K, VADIN M, VAUGHAN K, WATERSTON R., WATSON A, WINSTOCK L, WILKINSON-SPROAT J, WORLDMAN P, YOUNG M, ZHANG J.		Qy 539 LKEHFTENDVNTVIVENKAAYVNVYRDPFLRSGRILDFDIFRHFNPHEAR 598	
RA	Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.			Db 570 QSRHN 574
RN	[3]	SEQUENCE FROM N.A.		Qy 539 LKEHFTENDVNTVIVENKAAYVNVYRDPFLRSGRILDFDIFRHFNPHEAR 598
RP	SEQUENCE FROM N.A.			Qy 539 LKEHFTENDVNTVIVENKAAYVNVYRDPFLRSGRILDFDIFRHFNPHEAR 598
RA	WATENSTON R.			Db 570 QSRHN 574
RL	(PEB-1906) to the EMBL/GenBank/DBJ databases.			Qy 539 LKEHFTENDVNTVIVENKAAYVNVYRDPFLRSGRILDFDIFRHFNPHEAR 598
DR	BBM1: 050135; AAAS4453; 1. -.			Qy 539 LKEHFTENDVNTVIVENKAAYVNVYRDPFLRSGRILDFDIFRHFNPHEAR 598
DR	PROSTIE; PS00411; KINESIN_MOTOR_DOMAIN1; 1.			Db 570 QSRHN 574
DR	PPAFM; PP00229; Kinesin; 1.			Qy 539 LKEHFTENDVNTVIVENKAAYVNVYRDPFLRSGRILDFDIFRHFNPHEAR 598
DR	PPAFM; PE00169; PH; 1.			Db 570 QSRHN 574

SQ	SEQUENCE	689 AA:	77332 MW:	E43A1ED CRC32:
	Query Match	34.1%;	Score 1849;	DB 11;
	Best Local Similarity	51.3%;	Prev. 0.00e+00;	Length 689;
	Matches	329;	Conservative	130;
			Mismatches	128;
			Indels	56;
			Gaps	34;
Db	1	MGSC- YKAVYKVRPNNS ETSKKEKCTQNCQNSTLIP-	NP-K	-EPK 48
Qy	1	MGGGNKKVYKVRPNNAEIDORGAKCIVRREGQTILTPPAAEKKRSCKTMMGPK 60		
Db	49	SFSFDYWSHTSPEPDCASOSYRNDIGEMILHAFCGYNCCIFAYGOTGAGRSYMM 108		
Qy	61	AFAPDYSWYSEDFK- NAPN AFQDQFLQDGLPFLDAAFCGYNCCIFAYGOTGAGRSYMM 119		
Db	109	QKPEQESGAIQIPIPELKEFKIN-NCMDEQDNLHADLNLNPKNKRNLR 166		
Qy	120	GYKE-H-GYPIRICDMPRINELQDKNKCIVETVSYELEINERVDRDLPNSTGKLNK 177		
Db	167	TREPLAUGPVEDLISKLATVSTYSTDIAIDMAGKARVATANNEETSSSHAVPTVTFQ 226		
Qy	178	TREHPSGPVEDPELAKLVRVSQTEIENLMDGKARVATANNEETSSSHAVPTVTFQ 237		
Db	227	KKQDPETNLN-STEKVTKISYDLAGSERADSGAKGTRKLKGRIUNKLUTLGKVLSAEE 286		
Qy	238	KHDEDEKMPOTEVAKAISYDLAGSERADSGATGALKEGAEINNLSLTGRTVAAALAD 297		
Db	287	YSK-KKKKTDIFPQVSLTULLRNLGSRNTAVALSPADINDETLSTSRVATADR 345		
Qy	298	NSGQRKNNLVPIVYRUSVITWLLKUSLGLNMNTMAMIAISPAINTFPEITSLT-URADS 355		
Db	346	AQKOTPEVNLNAPVAKLREPEVTLKOLLAQOGLDIDNUKDFCQNNKHYLLASE 405		
Qy	356	AKRKNHAYVNEDPNARMRELKEPLAQLRKLQLOSS-GG--GG--AG----GSG 402		
Db	406	NORGNTSTASMSLISSSSSCSLNSQSGLTSVTSIORMSTPGGEAERLKEKSKII 465		
Qy	403	GPVEPSPPDN--PL-BKQV-SIG-QPD--A-T-YK-K-MSA--EVIGQNLSERY 448		
Db	466	AELNETWEEKLRKLTEAIRMERDALLAENGVAIRDEGDTLGCVSPKPTPOVNINLDPPLMS 525		
Qy	449	RDLAQNETWEEKLRKLTEAIRMERDALLAENGVAIRDEGDTLGCVSPKPTPOVNINLDPPLMS 506		
Db	526	ECLLYKDGDTIGTKEQQAERERDAALEEGIGIS-EKG-FVGPVHSKEMPHLYNSDGPIL 585		
Qy	507	ECLVNKGKQTVQ-ENVQDQAEFLRNGSKIKE-HCTF-E--NVDNV-VTVPNEK 559		
Db	586	SETYVNGVYRKAHPYQLRSRSTVSYWVKHNFVNHFNPHEQARARE 628		
Qy	560	RAVAVNGVYRKAHPYQLRSRSTVSYWVKHNFVNHFNPHEQARARE 602		
RESULT	7			
ID	001349	PRELIMINARY:	PRT:	1921 AA.
AC	001349;			
DT	01-JUL-1987	(T)EMBL.	04.	Created)
DT	01-JUL-1987	(T)EMBL.	04.	Last sequence update)
DT	01-NOV-1999	(T)EMBL.	12.	Last annotation update)
DE	KINESIN-73.			
OS	Drosophila melanogaster (Fruit fly)			
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;			
OC	PTerygota; Endopterygota; Diptera; Brachycera; Muscomorpha;			
OC	Ephydriidae; Drosophilidae; Drosophila.			
RN	[1]			
RP		SEQUENCE FROM N.A.		
RX		MEDLINE;		
RA		LIU H.P., LIU Z. M., NIRENBERG M.;		
RT		"Kinesin-73 in the nervous system of Drosophila embryos."		
RL		Proc. Natl. Acad. Sci. U. S. A. 94:1006-1091 (1997).		
DR		EMBL: U81788; AAB00464.1;		
DR		ELBbase: FB0019969; KINEC-73.		
DR		PROSITE: PS00411; KINESIN_MOTOR_DOMAIN1; 1.		
DR		PFAM: PF01302; CAP_GLY; 1.		
DR		DR		

1	MGRKDLSIVAVYRVPENDREKTRNCKLYVTEMPDRETTVTRDPKTDNEDEKRFYDHSYV-SH	59	RN	[5]
	PP	SEQUENCE FROM N.A.		
	RC	STRAIN-BRISTOL N2;		
	RA	WATERSTON R;		
	RL	Submitted (APR-1987) to the EMBL/GenBank/DBJ databases.		
2	MSGGGNIKVKVVRPENRAETDRGAKCIVRM-EGNOTILLPPGAEFEKARKSGKTIMDGP	59	DR	U1536; AAB52613.1; -.
3	DGTS-EKKRKYLEPTPFAODRGRFLDGGFLGRVLANAWAGYNSLQYQTSQSGSYSV	118	DR	HSSP; P3116; 1BG2.
4	60 KAFERDTSWFSKUNPAPYARQEDLFQQLGPFLDNAFKYNNCFAYQGTSQSGSYSV	119	DR	PROSITE: PS00411; KINESIN_1_MOTOR_DOMAIN1; 1.
5	119 GFKNKNGVIVTYQEFKQIAQ-NNKKMPEQEVYFMSMELCYKRDJLSSPPKGGLK	177	DR	PPM: PFO025; kinesin; 2.
6	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	PRINTS: PRO0380; KINESINHEAVY
7	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	KW	Motor protein; Microtubules; ATP-binding; Coiled coil.
8	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	SQ	SEQUENCE 1576 AA; 174409 MW; 80015D5C CRC32;
9	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	Score	20.7%; Score 1124; DB 5; Length 1576.
10	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	Query Match	20.7%; Score 1124; DB 5; Length 1576.
11	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	Best Local Similarity	54.5%; Pred. No. 1.18e-199; Indels 45; Gaps 19.
12	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	Matches	225; Conservative
13	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	8 SAYKVATYRKPENKEPBDLKTKSVYRIOEKCVL-HPP-LEEK- NS KT --- - PTF 55
14	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	5 GNIKVVVVRPNAEIDGKTCVRMEGNOTLTPPGAEBAFARSQGTTMDGKAFAF 64
15	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	56 DHFSCDTPHESDFTQSQTVEYLQGSEVNAEATGATFAYGQGCKSXYTMGTTDQ 115
16	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	65 DRSYWSFKDNAPNAYQARQDLSQDGLQVPLDNQAFGNNCI FAYGQGCKSXYSMGYGKE 124
17	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	66 PGJIPRVQNDITFRLQ-TSSNLSRPSYEMEYNNVYRVDLQPKSSKALKVRHEKKI 174
18	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	67 HGVIPRQCDQMPRINELQDKRNUCTIVSLEYTENYVDRDNLNSTKGKLN-KYKREPS 183
19	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	68 LGPMVQDLSILAVNSFEQI SMLLEGGKNSVTAATNNNAEESRSHAVFSLVYQTLHDL 234
20	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	69 184 TGPYVDELAKLKVYRVSFOEINEMDENGKAKRVAATNNNNETSSSHAEFTLTUQWHDDE 243
21	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	70 235 NGFSGEKVKASLVDLASSERAKTGAVGRLEGGNNIKNVLSIFLRDLKKTDEKFS 294
22	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	71 244 TKADETVAKISLVDLAAEATATGATGARLKEGAFTINSL-ST --- -L --- -G --- 290
23	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	72 295 ADYVFIFINOKLDFRSUTTIVGIVSALARNRKSNSRQFDSYVTLWKLDSGGSNSMIV 354
24	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	73 291 --- -V-TA --- -ALA --- DM --- SS-G-KQ-KNQVLPYFDSYVTLWKLDSGGSNSMIV 332
25	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	74 355 IATLSPAADNYVEETISLTLRDAYRDKVHNIAITINEDPNARV FEE REVEVTL 4 07
26	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	75 70 333 IAAISPADINFETLSTYRADSARXKHNAYDEFNARMLKEELAQIQR 385
27	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	76 71 RESULT 1.1
28	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	77 71 ID Q9Y495 PRELIMINARY; PRT; 702 AA.
29	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	78 71 AC Q9Y496; 01-NOV-1999 (TREMBL-1el, 12. Created)
30	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	79 71 DT 01-NOV-1999 (TREMBL-1el, 12. Last sequence update)
31	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	80 71 DT 01-NOV-1999 (TREMBL-1el, 12. Last annotation update)
32	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	81 71 DE KINESIN_FAMILY MEMBER PROTEIN KIF3A.
33	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	82 71 OS Homo sapiens (Human).
34	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	83 71 OC Eukaryota; Metazoa; Chordata; Craniata; Peleodrinae; Rhabditida; Rhabditina; Rhabditoidae; Rhabditidae; Caenorhabditis elegans.
35	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	84 71 OC Sequence from N.A.
36	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	85 71 OC SPAIN-BRISTOL N2;
37	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	86 71 OC WATERSHON R;
38	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	87 71 OC Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
39	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	88 71 OC SEQUENCE FROM N.A.
40	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	89 71 OC STRAIN-BRISTOL N2;
41	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	90 71 OC WATERSTON R;
42	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	91 71 OC Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
43	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	92 71 OC SEQUENCE FROM N.A.
44	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	93 71 OC STRAIN-BRISTOL N2;
45	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	94 71 OC WATERSTON R;
46	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	95 71 OC Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
47	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	96 71 OC SEQUENCE FROM N.A.
48	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	97 71 OC STRAIN-BRISTOL N2;
49	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	98 71 OC WATERSTON R;
50	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	99 71 OC Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
51	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	100 71 OC SPAIN-BRISTOL N2;
52	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	101 71 OC WATERSHON R;
53	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	102 71 OC Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
54	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	103 71 OC SEQUENCE FROM N.A.
55	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	104 71 OC SPAIN-BRISTOL N2;
56	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	105 71 OC WATERSHON R;
57	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	106 71 OC Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
58	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	107 71 OC SEQUENCE 193; Conservative
59	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	108 71 OC Matches 193; Conservative
60	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	109 71 OC SPAIN-BRISTOL N2;
61	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	110 71 OC WATERSHON R;
62	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	111 71 OC Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
63	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	112 71 OC SEQUENCE FROM N.A.
64	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	113 71 OC STRAIN-BRISTOL N2;
65	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	114 71 OC WATERSTON R;
66	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	115 71 OC Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
67	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	116 71 OC SPAIN-BRISTOL N2;
68	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	117 71 OC WATERSHON R;
69	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	118 71 OC Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
70	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	119 71 OC SEQUENCE FROM N.A.
71	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	120 71 OC SPAIN-BRISTOL N2;
72	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	121 71 OC WATERSHON R;
73	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	122 71 OC Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
74	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	123 71 OC SEQUENCE FROM N.A.
75	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	124 71 OC SPAIN-BRISTOL N2;
76	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	125 71 OC WATERSHON R;
77	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	126 71 OC Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
78	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	127 71 OC SEQUENCE FROM N.A.
79	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	128 71 OC SPAIN-BRISTOL N2;
80	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	129 71 OC WATERSHON R;
81	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	130 71 OC Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
82	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	131 71 OC SEQUENCE FROM N.A.
83	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	132 71 OC SPAIN-BRISTOL N2;
84	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	133 71 OC WATERSHON R;
85	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	134 71 OC Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
86	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	135 71 OC SEQUENCE FROM N.A.
87	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	136 71 OC SPAIN-BRISTOL N2;
88	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	137 71 OC WATERSHON R;
89	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	138 71 OC Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
90	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	139 71 OC SEQUENCE FROM N.A.
91	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	140 71 OC SPAIN-BRISTOL N2;
92	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	141 71 OC WATERSHON R;
93	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	142 71 OC Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
94	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	143 71 OC SEQUENCE FROM N.A.
95	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	144 71 OC SPAIN-BRISTOL N2;
96	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	145 71 OC WATERSHON R;
97	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	146 71 OC Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
98	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	147 71 OC SEQUENCE FROM N.A.
99	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	148 71 OC SPAIN-BRISTOL N2;
100	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	149 71 OC WATERSHON R;
101	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	150 71 OC Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
102	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	151 71 OC SEQUENCE FROM N.A.
103	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	152 71 OC SPAIN-BRISTOL N2;
104	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	153 71 OC WATERSHON R;
105	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	154 71 OC Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
106	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	155 71 OC SEQUENCE FROM N.A.
107	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	156 71 OC SPAIN-BRISTOL N2;
108	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	157 71 OC WATERSHON R;
109	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	158 71 OC Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
110	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	159 71 OC SEQUENCE FROM N.A.
111	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	160 71 OC SPAIN-BRISTOL N2;
112	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	161 71 OC WATERSHON R;
113	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	162 71 OC Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
114	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	163 71 OC SEQUENCE FROM N.A.
115	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	164 71 OC SPAIN-BRISTOL N2;
116	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	165 71 OC WATERSHON R;
117	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	166 71 OC Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
118	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	167 71 OC SEQUENCE FROM N.A.
119	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	168 71 OC SPAIN-BRISTOL N2;
120	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	169 71 OC WATERSHON R;
121	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	170 71 OC Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
122	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	171 71 OC SEQUENCE FROM N.A.
123	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	172 71 OC SPAIN-BRISTOL N2;
124	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	173 71 OC WATERSHON R;
125	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	174 71 OC Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
126	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	175 71 OC SEQUENCE FROM N.A.
127	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	176 71 OC SPAIN-BRISTOL N2;
128	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	177 71 OC WATERSHON R;
129	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	178 71 OC Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
130	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	179 71 OC SEQUENCE FROM N.A.
131	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	180 71 OC SPAIN-BRISTOL N2;
132	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	181 71 OC WATERSHON R;
133	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	182 71 OC Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
134	120 GYKKEHQVTPRQDMRQMLNQDKNLTCTVEYLEYNERVDRLN-PSKGRLK	177	DR	183 71 OC

Qy	6	NIKVYVRPENAREIDRGAKCIVRMEGRQTLPPGAEERAKSGKTTMDPRAFAED	Db	169	RFDIGVYKQDLSFTVSYKEIEHVNNGVNQNSGVATMNEHSSRAIFKMITI - E-CSO 227
Db	65	-T--VP--GPE-SKOLDY-NL-NIATPDSVYGLSYGNTTIFYGTGTTGTTMGTGVT 116	Qy	181	HSTPQYVDELAKVYRSPQFQINLMDCEKNTVATVATMNETTSRSHAVFTLTOKHH 240
Db	66	RSTWEDKNAANARQDLEDFDLYV PLDNaFQYKNTNIFYGTGCKSISMSMGY - GK 123	Db	228	IGLDGENHIVRKGKLNIVDLAGSERQTKGQERGLKEAKTINLSLALGIVNISALVD-- 284
Db	117	PELGTPINSPAHIFGHTAKAEGTQFL - VRVSYLETNEYVERDUGKQCTORLAYERK 174	Qy	241	DEETMMDTEKVANISWDLAGSERATGARLAEQEAEINSLSTGRVTAALADMSS 300
Qy	124	-B-HGIVPRICDQMFNRNELQDKNUTCTEVSYLETNEYVERDUNSTGALKYREH 181	Db	285	GR -STH-IVPQSKATLQDLSFGNATKTMANGVATWANGPANVEETLTPLRSARWIK 341
Db	175	PDGYTPTKDISAVYVNNADDNDR-IMTGLKHSRGTGNTNHEUHSRSIAITPTTICKERK 234	Qy	301	GROKNNQVPPYRQSVLTLKQDGNSNTMAMIAISPADINEETLSTLRTADSARIK 360
Qy	182	PSTGPVYEDLAKLKVRSFQEINLMDGEKARTVATYNNETSSHAYFTLJLQRWHD 241	Db	342	NKFRYNEPDADLRFQEBETARAKQDLKQVG 374
Db	235	IDGNHRY - RMRKHLVLDLGSERDAGTGTGQRLKEAKTINUSLGTGIVNISALVD--G 250	Qy	361	NIHAVVNPARNIRLEKELAQLRSKLQSGG 393
Qy	242	BETKMDTVERAKTISVLDLGSERDAGTGTGQRLKEAKTINUSLGTGIVNISALVDSSG 301			
Db	291	K -STH -VPRNKLTRLQDLSGKNTMCANTGPDAYNDETISTLYRANRANKN 347	RESULT 13		
Qy	302	KOKKNQLPYDVSYLNWLLKQSGMSMTAATSPAINTEETLSTLRYAADSARKRN 361	ID 018389	PRELIMINARY;	PRT; 1121 AA.
Db	348	KARINEDPKDALARQFQETELKLUKB - GRESESSDTSGSEEDDDEGEYGEGERGKRR 406	AC 018389		
Qy	362	HAYVNEDPNAHNPBEKELFQELQKLSQSSGCGGCGGCGCQVSEYKPPDPLKQVS 421	AC 01-JAN-1998 (T-EMBL) 05	Created)	
Db	407	KRQIQGKVKVSPDKMIE-QA-KIDEE -RKALETKLDEEEERNKARAK 455	DT 01-JAN-1998 (T-EMBL) 05	Last sequence update)	
Qy	422	IQQDPTVKKNSKAETEVLNOSEKFLRDLNOTWEEKLAKTEIHKEREALE 474	DT 01-NOV-1998 (T-EMBL) 12	Last annotation update)	
RP		SEQUENCE FROM N_A.	DR		
RP		SEQUENCE FROM N_A.	DR		
RP		SEQUENCE FROM N_A.	DR		
AC	094478	PRELIMINARY; PRT; 744 AA.	DR		
AC	094478	PRELIMINARY; PRT; 744 AA.	DR		
DT	01-NOV-1998 (TREMBL) 08; Last sequence update)	DR			
DT	01-NOV-1998 (TREMBL) 08; Last sequence update)	DR			
DT	01-NOV-1998 (TREMBL) 12; Last annotation update)	DR			
DE	KINESIN_LIKE_PROTEIN 3.	DR			
GN	XKIP3.	DR			
OS	Xenopus laevis (African clawed frog)	DR			
CC	Bukit Jaya; Metacida; Chordata; Cratata; Vertebrata; Amphibitis;	DR			
CC	Batrachia; Anura; Mesobatrachia; Pipidae; Xenopodinae;	DR			
CC	Xenopus.	DR			
RP	SEQUENCE FROM N_A.	DR			
RX	MEDLINE: 9316055.	DR			
RA	VERNOIS I., HEASMAN J., WYLIE C.;	DR			
RT	"Multiple kinesin-like transcripts in Xenopus oocytes.";	DR			
RL	Dev. Biol. 157:232-239 (1993).	DR			
RN	[2]	SEQUENCE FROM N_A.	DR		
RP	SEQUENCE FROM N_A.	DR			
RA	LE BOU N., ANTONY C., WHITE J., KARSENTI S., VERNOS I.:	DR			
RT	*Role of Xklb3, a subunit of Xenopus kinesin II hetero-imeric	DR			
RT	complex in membrane transport at the ER/Golgi interface. *	DR			
RL	Submitted: 2001-08-19 09:00:00; Last update: 2001-08-19 09:00:00.	DR			
EMBL	Accession: EMBL: A500893; CAA08973.1;	DR			
PROSITE	PS00411; KINESIN_MOTOR_DOMAIN1; 1.	DR			
PRINTS	PRO380; KINESIN_HAve.	DR			
KW	Motor protein; Microtubules; ATP-binding; Colled coll.	DR			
SO	SEQUENCE FROM N_A.	DR			
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RT	*Role of Xklb3, a subunit of Xenopus kinesin II hetero-imeric	DR			
RT	complex in membrane transport at the ER/Golgi interface. *	DR			
RL	Submitted: 2001-08-19 09:00:00; Last update: 2001-08-19 09:00:00.	DR			
EMBL	Accession: EMBL: A500893; CAA08973.1;	DR			
PROSITE	PS00411; KINESIN_MOTOR_DOMAIN1; 1.	DR			
PRINTS	PRO380; KINESIN_HAve.	DR			
KW	Motor protein; Microtubules; ATP-binding; Colled coll.	DR			
SO	SEQUENCE FROM N_A.	DR			
RX	VERNOIS I., HEASMAN J., WYLIE C.;	DR			
RT	"Multiple kinesin-like transcripts in Xenopus oocytes.";	DR			
RL	Dev. Biol. 157:232-239 (1993).	DR			
RN	[2]	SEQUENCE FROM N_A.	DR		
RP	SEQUENCE FROM N_A.	DR			
RA	LE BOU N., ANTONY C., WHITE J., KARSENTI S., VERNOS I.:	DR			
RT	*Role of Xklb3, a subunit of Xenopus kinesin II hetero-imeric	DR			
RT	complex in membrane transport at the ER/Golgi interface. *	DR			
RL	Submitted: 2001-08-19 09:00:00; Last update: 2001-08-19 09:00:00.	DR			
EMBL	Accession: EMBL: A500893; CAA08973.1;	DR			
PROSITE	PS00411; KINESIN_MOTOR_DOMAIN1; 1.	DR			
PRINTS	PRO380; KINESIN_HAve.	DR			
KW	Motor protein; Microtubules; ATP-binding; Colled coll.	DR			
SO	SEQUENCE FROM N_A.	DR			
RX	VERNOIS I., HEASMAN J., WYLIE C.;	DR			
RT	"Multiple kinesin-like transcripts in Xenopus oocytes.";	DR			
RL	Dev. Biol. 157:232-239 (1993).	DR			
RN	[2]	SEQUENCE FROM N_A.	DR		
RP	SEQUENCE FROM N_A.	DR			
RA	LE BOU N., ANTONY C., WHITE J., KARSENTI S., VERNOS I.:	DR			
RT	*Role of Xklb3, a subunit of Xenopus kinesin II hetero-imeric	DR			
RT	complex in membrane transport at the ER/Golgi interface. *	DR			
RL	Submitted: 2001-08-19 09:00:00; Last update: 2001-08-19 09:00:00.	DR			
EMBL	Accession: EMBL: A500893; CAA08973.1;	DR			
PROSITE	PS00411; KINESIN_MOTOR_DOMAIN1; 1.	DR			
PRINTS	PRO380; KINESIN_HAve.	DR			
KW	Motor protein; Microtubules; ATP-binding; Colled coll.	DR			
SO	SEQUENCE FROM N_A.	DR			
RX	VERNOIS I., HEASMAN J., WYLIE C.;	DR			
RT	"Multiple kinesin-like transcripts in Xenopus oocytes.";	DR			
RL	Dev. Biol. 157:232-239 (1993).	DR			
RN	[2]	SEQUENCE FROM N_A.	DR		
RP	SEQUENCE FROM N_A.	DR			
RA	LE BOU N., ANTONY C., WHITE J., KARSENTI S., VERNOS I.:	DR			
RT	*Role of Xklb3, a subunit of Xenopus kinesin II hetero-imeric	DR			
RT	complex in membrane transport at the ER/Golgi interface. *	DR			
RL	Submitted: 2001-08-19 09:00:00; Last update: 2001-08-19 09:00:00.	DR			
EMBL	Accession: EMBL: A500893; CAA08973.1;	DR			
PROSITE	PS00411; KINESIN_MOTOR_DOMAIN1; 1.	DR			
PRINTS	PRO380; KINESIN_HAve.	DR			
KW	Motor protein; Microtubules; ATP-binding; Colled coll.	DR			
SO	SEQUENCE FROM N_A.	DR			
RX	VERNOIS I., HEASMAN J., WYLIE C.;	DR			
RT	"Multiple kinesin-like transcripts in Xenopus oocytes.";	DR			
RL	Dev. Biol. 157:232-239 (1993).	DR			
RN	[2]	SEQUENCE FROM N_A.	DR		
RP	SEQUENCE FROM N_A.	DR			
RA	LE BOU N., ANTONY C., WHITE J., KARSENTI S., VERNOS I.:	DR			
RT	*Role of Xklb3, a subunit of Xenopus kinesin II hetero-imeric	DR			
RT	complex in membrane transport at the ER/Golgi interface. *	DR			
RL	Submitted: 2001-08-19 09:00:00; Last update: 2001-08-19 09:00:00.	DR			
EMBL	Accession: EMBL: A500893; CAA08973.1;	DR			
PROSITE	PS00411; KINESIN_MOTOR_DOMAIN1; 1.	DR			
PRINTS	PRO380; KINESIN_HAve.	DR</			

Qy 209 GKHATVAAHNNEYSISHAVT--LUTQ-KWHD---B-ETKMDTE-K-V--AKISL 256
 Db 409 VDLASERIVSGNSCERIREGVTSNKSLTGKVIAALASRSKATANGPLGCTPSTEV 468
 Qy 257 VDLASERATSGATGARKEGAENRLSLTRVAALAD---NSOKQ-K-NOLY 309
 Db 469 PYRESVTLRNLNGNSKTYMLATISPAISIHAETATLRYACFARBYNWKYNESP 528
 Qy 310 PYRESVTLRNLNGNSKTYMLATISPAISIHAETATLRYACFARBYNWKYNESP 369
 Db 529 HOKITRORAYDRKLX-LANEYERORL--SGNS-NNPVERALLET--SVDETE--V 579
 Qy 370 NARMRELKELAQRSLAOSLSSGGGAGGGPVESEYPDPERQIVSIQODAVV 429
 Db 580 EAL-ROOLABR--ERE-LSRA-OKSMKLUKEEDORKSBLVLRKGIALE--LTAE-Q 631
 Qy 430 KMSKABEVOLNQSEKLYRDLMQWEKLAKTEELKREBAALEPLGISTERFVGPH 489
 Db 632 -KO-ACLVNUTADPLSOTFLYLLPQVYTRGRPLGSSSSQDPIVLDQPLQHCS 689
 Qy 490 SREMPHLVNLISDPLAELCYVINGPQTRVG N-V--NNDQTAIRUNGSKLEHCT 544
 Db 690 IERHGGKLIVIPGSEDEFYVNGLLEDRQFLPHGDMLVIGGSHYFRSLNP 741
 Qy 545 FENV-DNVTIYF-NEKAAMVNGYRDKPTRLRSYRILGDFHIFRNP 594

Search completed: Mon Aug 21 15:42:14 2000
 Job time : 66 secs.

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XX Sequence 3, Application US/08713815A
 XX Sequence 3, Application US/08713815A
 CC Patent No. 5830639
 CC GENERAL INFORMATION:
 CC APPLICANT: Russell J. Stewart
 CC TITLE OF INVENTION: ACTIVE MICROTUBE-BASED
 CC NUMBER OF SEQUENCES: 6
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESS: Thorpe, No. 5830659th & Western, L.I.P.
 CC STREET: 9035 South 700 East, Suite 200
 CC CITY: Sandy
 CC STATE: Utah
 CC COUNTRY: USA
 CC ZIP: 84070
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage
 CC COMPUTER: AST Ascentia 900N
 CC OPERATING SYSTEM: DOS 6.22
 CC SOFTWARE: Word Perfect 6.0
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/08/713.815A
 CC FILING DATE: 13 SEP 1996
 CC CLASSIFICATION: 35
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Alan J. Howarth
 CC REFERENCE/DOCKET NUMBER: 36-5553
 CC REGISTRATION NUMBER: T214/0-2202
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: (801)566-6633
 CC TELEFAX: (801)566-0750
 CC INFORMATION FOR SEQ ID NO: 3:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 441 amino acid residues
 CC TYPE: amino acid
 CC TOPOLOGY: linear
 CC SEQUENCE: 441 AA: 48936 MW: 924366 CN:
 CC
 Query Match Similarity 13.0%; Score 707; DB 2; Length 441;
 Best Local Similarity 42.3%; Pred. No. 5.23e-45;
 Matches 138; Conservative 77; Mismatches 91; Indels 20; Gaps 12;

Db 55 FDWRKPHASDEVKRYVREAKSIVDYLADGSTNTFAYGOTSSKGTHMAGSVAIGDSVQKGI 114
 Qy 71 FDNRNAYTAROFLDQGVLNDFQKAFYKNCYFAYGQGKSYWAG-IGKSV--HGV 127
 Sq
 Db 115 IPRVNDIFHIVYAM-EVNLIEFHIVKSYTEYMDKIRDLDEVS-KYNSLVDENRIVPY 171
 Qy 128 IPRICODMFRIANLQDKNUCTIVSYLLEYNVRDILPSKGNKVRHEHSTGPY 187
 Db 172 VKADEFERVSPDPEVIEFGRGSKHNTVANMEISSHVELVINKOENLEROKKL- 230
 Qy 188 VEDLAKLIVRSPDPEVIEFGRGSKHNTVANMEISSHVELVINKOENLEROKKL- 247
 Db 231 S---GKLVLDLQGSKYKSYKIGVDEAKNINNSBALGNTVISALD--GN--KTH 282
 Qy 248 TERYAKISLVLGASRSATSGTARLKEAENSLSTLGRYTAALMSGQKQKNG 307
 Db 283 -TPYDSDLRLQESLGNNARTIVCCSPASINSEKSTLDFGRAKTNYVCYNE 341
 Qy 308 LPYDSDLRLQESLGNNARTIVCCSPASINSEKSTLDFGRAKTNYVCYNE 367
 Db 342 ELTAEBKRYKEKEKVNARLKGKV 367
 Qy 368 D--PNMRIR-EL--KEELAQLRSKLQ 389

RESULT 9
 ID US-08-345-860D-48
 XX STANDARD: PRT; 1612 AA.
 AC XXXXXX

XX Sequence 48, Application US/08545860D
 CC Sequence 48, Application US/08545860D
 CC Patent No. 600140
 CC GENERAL INFORMATION:

Db	442	VVTTTPPSMADTYEGORISPTMLOGKVKVFGASHVPEKFDPSQDHA	491
Qy	551	VVTIVPERAAVN-VNGYRDRPLRSGYRILGDFHFRNPEEARA	599
RESULT	10		
ID	US 08 695-871 2	STANDARD;	PRT;
XX			1354 AR.
AC	xxxxx		
XX			
DT			
XX			
DE			
XX			
CC	Sequence 2, Application US/08685871		
CC	Patent No. 6013499		
CC	GENERAL INFORMATION:		
CC	APPLICANT: NARUMIYA, Akihiro		
CC	APPLICANT: IWANAMI, Shuh		
CC	TITLE OF INVENTION: RHO TARGET PROTEIN KINASE p160		
CC	NUMBER OF SEQUENCES: 68		
CC	CORRESPONDENCE ADDRESS:		
CC	ADDRESSEE: Foley & Lardner		
CC	STREET: 3000 K Street, N.W., Suite 500		
CC	CITY: Washington		
CC	STATE: D.C.		
CC	COUNTRY: USA		
CC	ZIP: 20007-5109		
CC	COMPUTER READABLE FORM:		
CC	MEDIUM TYPE: FLOPPY DISK		
CC	COMPUTER: IBM PC compatible		
CC	OPERATING SYSTEM: PC-DOS/MS-DOS		
CC	SOFTWARE: Patentus Release 11.0, Version # 1.30		
CC	CURRENT APPLICATION DATA:		
CC	APPLICATION NUMBER: US/08/685,871		
CC	FILING DATE: 24-JUL-1996		
CC	CLASSIFICATION: 435		
CC	PRIOR APPLICATION DATA:		
CC	APPLICATION NUMBER: JP 9-184102		
CC	FILING DATE: 15-JUN-1996		
CC	PRIOR APPLICATION DATA:		
CC	APPLICATION NUMBER: JP 7-262553		
CC	FILING DATE: 14-SEP-1995		
CC	ATTORNEY/AGENT INFORMATION:		
CC	NAME: BENT, Stephen A.		
CC	REGISTRATION NUMBER: 29,768		
CC	REFERENCE/DOCKET NUMBER: 16887/845		
CC	TELECOMMUNICATION INFORMATION:		
CC	TELEPHONE: (202)672-5300		
CC	TELEFAX: (202)672-5399		
CC	TELEX: 904136		
CC	INFORMATION FOR SEQ ID NO: 2:		
CC	SEQUENCE CHARACTERISTICS:		
CC	LENGTH: 1354 amino acids		
CC	TYPE: amino acid		
CC	TOPOLOGY: linear		
CC	MOLECULE TYPE: protein		
CC	SEQUENCE: 1354 AA: 158174 MW: 8778645 CN:		
CC	Query Match Similarity: 2.28%; Score: 120; DB: 3; Length: 1354;		
CC	Best Local Matches: 41; Pred. Similarity: 28.1%; Pred. Score: 2.95e-00; Smatches: 66; Indels: 7		
Db	849	EQYFSIUYTQTQVKELKEEDEKARNEKIQOLQNEKETLATQDLETRAESEB	
Qy	344	ETULSTLRYADSRSKRNHAYVNEDPARNMREKELAQLRSKQSSGGGGAA	
Db	908	LLEEQYETUQESKRAKSNRQETDQDHTVSRLBANSMLTKDTEIURR-NPE	
Qy	404	PVEESYPDPDPLKQVSYTQPDATVK--RMSKAELVEQ-LNQS-EKLYRNLQG	
Db	967	KKAAPEEELKEPEELSNKKAAPEKNTI	992

QY 460 AKTEETH-EREAALBELGIESTEKGFP 484

RESULT 11 Sequence 30, Application PC/TUS9414030A

ID US-08-785-310A-6 STANDARD; PRT; 594 AA.

XX

AC xxxxxx

XX

DT

XX

DE Sequence 6, Application US/08785310A

XX

CC Sequence 6, Application US/08785310A

CC GENERAL INFORMATION:

CC ID: 580532

CC COMPUTER: IBM PC compatible

CC NUMBER OF SEQUENCES: 8

CC TITLE OF INVENTION: Neuronal PAS Domain Protein

CC ADDRESSEE: SCIENCE 6 TECHNOLOGY LAW GROUP

CC STREET: 268 BUSH STREET, SUITE 3200

CC CITY: SAN FRANCISCO

CC STATE: CALIFORNIA

CC COUNTRY: USA

CC ZIP: 94101

CC COMPUTER READABLE FORM:

CC COMPUTER: IBM PC compatible

CC OPERATING SYSTEM: PC-DOS/MS-DOS

CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: US/08/785, 310A

CC FILING DATE: 21-JAN-1997

CC CLASSIFICATION: 536

CC ATTORNEY/AGENT INFORMATION:

CC NAME: OSMAN, RICHARD A.

CC REGISTRATION NUMBER: 36, 627

CC REFERENCE/DOCKET NUMBER: US/SD-1226

CC TELECOMMUNICATION INFORMATION:

CC TELEPHONE: (415) 343-4342

CC INFORMATION FOR SEQ ID NO: 6:

CC SEQUENCE CHARACTERISTICS:

CC LENGTH: 594 amino acids

CC STRANDEDNESS: single

CC TOPOLOGY: linear

CC MOLECULE TYPE: Peptide

SQ SEQUENCE 594 AA: 63736 MW: 1871071 CN;

Query Match 1. 9% Score 101; DB 2; Length 594;

Best Local Similarity 20.0%; Pred No. 4, 45e-01;

Matches 19; Conservative 27; Mismatches 4; Indels 2; Gaps 2;

RESULT 13 Sequence 30, Application US/08362670B

DB 174 QVELGSSVVEDYIHPGD-HSVEIQLGRASITGPPPPVPSVSSSSSIIVDPELEA 232

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QY 590 RILIDDFIIPRHPPEAARQQLRHSYNTSOLGSPAPGRHDRTLKSAGSDAGDS 639

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Db 233 SPTEASPAFRAQR-SFTYRKSTKLKGRLKAVAS 266

QY 640 RSDSPLPFNGKSDMFTARAEASIGLQKTS 674

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RESULT 12 Sequence 30, Application US/08362670B

ID PC/TUS94-14030A-30 STANDARD; PRT; 240 AA.

XX

AC xxxxxx

XX

DT

XX

DE Sequence 30, Application PC/TUS9414030A

XX

CC GENERAL INFORMATION:

CC APPLICANT: GENETICS INSTITUTE, INC.

CC PRESIDENT AND FELLOWS OF HARVARD COLLEGE

CC TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS

CC NUMBER OF SEQUENCES: 35

CC CORRESPONDENCE ADDRESS:

CC GENETICS INSTITUTE, INC.

STREET: 87 Cambridgepark Drive

CITY: Cambridge

STATE: Massachusetts

CC COUNTRY: USA

CC ZIP: 02140

CC COMPUTER READABLE FORM:

CC COMPUTER: IBM PC compatible

CC OPERATING SYSTEM: PC-DOS/MS-DOS

CC SOFTWARE: PatentIn Release #1.0, Version #1.25

CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: PC/TUS94/14030A

CC ATTORNEY/AGENT INFORMATION:

CC FILING DATE: Herewith

CC CLASSIFICATION:

NAME: Lazaf, Steven R.

CC PRIORITY APPLICATION DATA:

CC APPLICATION NUMBER: US 08/164, 103

CC FILING DATE: 07-DEC-1993

CC APPLICATION NUMBER: US 08/217, 780

CC FILING DATE: 25-MAR-1994

CC APPLICATION NUMBER: US 08/333, 576

CC FILING DATE: 02-NOV-1994

CC ATTORNEY/AGENT INFORMATION:

CC REFERENCE/DOCKET NUMBER: 5202D-PC*

CC TELECOMMUNICATION INFORMATION:

CC TELEPHONE: 617 498-8260

CC TELEFAX: 617 876-5851

CC INFORMATION FOR SEQ ID NO: 30:

CC SEQUENCE CHARACTERISTICS:

CC LENGTH: 240 amino acids

CC TYPE: amino acid

CC MOLECULE TYPE: Protein

SQ SEQUENCE 240 AA: 24846 MW: 262270 CN;

Query Match 1. 8% Score 95; DB 4; Length 240;

Best Local Similarity 51.7%; Pred. No. 1.0e-02;

Matches 15; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

DB 91 RRQRIPLAIGTRGXGSGGGGGGGGGGGGG 119

QY 375 RELKEELAQLRSKLQSSGGGGGGGGGG 403

RESULT 13 Sequence 30, Application US/08362670B

XX

XX

XX

XX

XX

XX

CC GENERAL INFORMATION:

CC ID: 5688682

CC PATENT NO. 5688682

CC ATTORNEY/AGENT INFORMATION:

CC CELESTE, Anthony J.

CC APPLICANT: Celeste, Anthony J.

CC ROZNEY, John

CC APPLICANT: Rozney, John

CC ROSEN, Vicki A.

CC APPLICANT: Rosen, Vicki A.

CC WOLMAN, Neil

CC APPLICANT: Wolman, Neil

CC THOMSEN, Gerald H.

CC APPLICANT: Thomsen, Gerald H.

CC MELTON, Douglas A.

CC APPLICANT: Melton, Douglas A.

CC TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS

CC NUMBER OF SEQUENCES: 37

CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: GENETICS INSTITUTE, INC.
 CC STREET: 87 CambridgePark Drive
 CC CITY: Cambridge
 CC STATE: Massachusetts
 CC COUNTRY: USA
 CC ZIP: 02140

CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC Compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Patent Release #1.0. Version #1.25
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/08/362,670B
 CC FILING DATE: December 22, 1994
 CC CLASSIFICATION: 514
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: LIZZI, Steven P.
 CC REGISTRATION NUMBER: 32,618
 CC REFERENCE/DOCKET NUMBER: 5202-D
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: 617 438-5260
 CC TELEFAX: 617 876-5851
 CC INFORMATION FOR SEQ ID NO: 30:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 240 amino acids
 CC TYPE: amino acid
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: protein
 CC SEQ ID NO: 24846 MN: 262270 CN:
 CC SEQUENCE 240 AA:
 Query Match Similarity 1.8%; Score 95; DB 1; Length 241
 Best Local Matches 51.7%; Pred. No. 1.0e+02;
 Matches 15; Conservative 5; Mismatches 9; Indels 0

Db 91 RQRDTAQLAGRGXGSGGGGGGGGGGGGGGG 119
 Qy 375 RELKEELAQLRSKLQSSGGGGGGGGGG 403

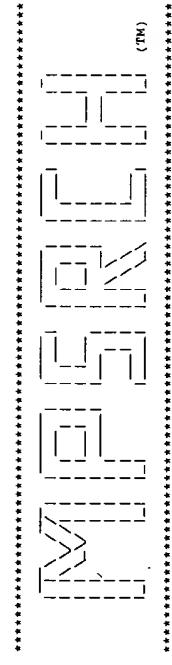
RESULT -14
 ID US-08-333-576C-30
 XX
 XX
 AC
 XX
 DT
 XX

Sequence 30, Application US/08333576C
 Sequence 30, Application US/08333576C
 Patent No. 6,027,919
 GENERAL INFORMATION:
 APPLICANT: Celeste, Anthony J.
 APPLICANT: Rooney, John
 APPLICANT: Vicki A.
 APPLICANT: Wolfman, Neil A.
 APPLICANT: Thomson, Gerald H.
 APPLICANT: Melton, Douglas A.
 TITLE OF INVENTION: TENDON-INDUCING COMPOSITIONS
 NUMBER OF SEQUENCES: 37
 CURRENT ADDRESS:
 ADDRESSEE: GENETICS INSTITUTE, INC.
 STREET: 87 CambridgePark Drive
 CITY: Cambridge
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02140

CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC Compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Patent Release #1.0. Version #1.25
 CC CURRENT APPLICATION DATA:

Search completed: Mon Aug 21 15:42:50 2000
Job time : 19 secs.

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Release 3.1A John F. Collins, Biocomputing Research Unit.

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Distribution rights by Oxford Molecular Ltd

MSEARCH_PP protein - Protein database search, using Smith-Waterman algorithm

Run on: Mon Aug 21 15:38:36 2000; MasPar time 22.31 Seconds

Tabular output not generated.

Title: >US-09-235-416-1

Description: (1.78) from US09235416A, pep

Perfect Score: 5422

Sequence: 1 MGGGNKVKVVRVPNARE.....ELRQQAQMEALKTAQEF 784

Scoring table: PAM 150

Post-processing: Minimum Match 0^a

Gap 11

Searched: 189963 seqs., 23686106 residues

Post-processing: Minimum Match 0^a

Gap 11

Listing first 45 summaries

Database: a-geneseq36

1:geneseqP

Statistics: Mean 37.958; Variance 188.559; scale 0.201

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match Length	DB ID	Description	Pred. No.
1	953	17.6	955	Leishmania chagasi K39	5.5e-67
2	953	17.6	955	Leishmania chagasi K39	5.5e-67
3	791	14.6	2954	R57651	5.5e-67
4	707	13.0	411	Y01632	5.5e-67
5	707	13.0	441	W72446	2.4e-16
6	707	13.0	441	W72446	2.4e-16
7	509	9.4	324	W70335	5.8e-16
8	424	7.8	679	W88456	4.7e-13
9	211	3.9	1201	W90456	2.1e-05
10	196	3.6	1612	W2494	2.6e-05
11	195	3.6	1612	R66457	2.6e-05
12	193	3.4	1899	Y0742	2.6e-04
13	120	2.2	1334	107982	5.1e-04
14	120	2.2	1334	W1202	5.1e-04
15	120	2.2	1354	W23554	5.1e-04
16	113	2.1	350	Y13384	5.1e-04
17	113	2.1	350	W22995	1.4e-01
18	106	2.0	235	W22995	1.4e-01
19	108	2.0	320	P94666	41KD protein of T. col
20	107	2.0	349	W73016	3.9e-01
21	108	2.0	350	W73016	Mouse cysteine-rich se
22	106	2.0	857	K97702	2.9e-01
23	107	1.1	109	R19197	Staphylococcus aureus C5G protein.

24	106	2.0	1464	W42632	Human transcriptional Mutant GC4 oligomer.
25	101	1.9	66	W22020	Single chain antibody
26	102	1.9	243	W60769	Protein activated 11p
27	101	1.9	339	F77317	Interferon alpha - immun
28	104	1.9	433	W18579	Human P53 protein vari
29	102	1.9	535	W228491	Human B5 protein vari
30	102	1.9	535	W28492	FULL-length C60 bindi
31	102	1.9	567	W39559	Mouse neuronal PAS dom
32	101	1.9	594	W68192	Streptococcus pneumoniae
33	102	1.9	605	W48378	Romo sapiens don-1 pol
34	103	1.9	647	W48378	6.0e-01
35	104	1.9	1463	W99482	Murine NC42 protein
36	102	1.8	3054	F40841	Translation of TEV lar
37	100	1.8	50	W3633	Acidic ribosomal antige
38	100	1.8	371	F883015	Human thyroid transi
39	100	1.8	425	W08621	S. pneumoniae protein
40	100	1.8	430	W01287	9.15e-01
41	100	1.8	442	F79033	Nuclear inclusion prot
42	100	1.8	924	W60161	Human intercellular ad
43	100	1.8	924	W09031	Human ICAM-4
44	100	1.8	924	W5006	Human ICAM-4 protein
45	100	1.8	924	W73511	Human neuronal ICAM-4

ALIGNMENTS

RESULT¹ standard; Protein: 955 AA.

ID W03621; AC W03621;

DT 05-MAR-1997 (first entry)

DE Leishmania chagasi; K39 antigen.

KW epitope: K39

CCP

CC compounds including polypeptides that contain at least an epitope of

CC the L. chagasi acidic ribosomal antigen. These are useful in variety

CC of immunoassays for detecting Leishmania infection. Portions of

CC the Lcp0 ("T42166") contg. at least the 17-terminal amino acids (T42165)

CC have been found to generate a signal in an ELISA that is equivalent

CC to that generated by the full length Lcp0. A combination

CC of peptide may also be used, comprising an Lcp0 epitope along with

CC an epitope derived from the Leishmania K99 antigen (T2166), pref.

CC the K99 repeat unit antigen having the sequence given in W03620.

CC sequence: 955 AA;

SQ

Q933: DB 1; Length 955;

P933: Pred. No. 5.54e-67;

R933: 90; Mismatches 11; Indels 29; Gaps 18;

S933: 17; Local Similarity 43.58%; Conservative 177; Matches 90;

T933: 7 IVKVRPRNAEKGTVYQANAVVTPYKLGSSNNAAEASGTRRYAD 72

U933: 7 IVKVRPRNAEKGTVYQANAVVTPYKLGSSNNAAEASGTRRYAD 72

V933: 7 IVKVRPRNAEKGTVYQANAVVTPYKLGSSNNAAEASGTRRYAD 72

W933: 7 IVKVRPRNAEKGTVYQANAVVTPYKLGSSNNAAEASGTRRYAD 72

X933: 7 IVKVRPRNAEKGTVYQANAVVTPYKLGSSNNAAEASGTRRYAD 72

Y933: 7 IVKVRPRNAEKGTVYQANAVVTPYKLGSSNNAAEASGTRRYAD 72

Z933: 7 IVKVRPRNAEKGTVYQANAVVTPYKLGSSNNAAEASGTRRYAD 72

A933: 7 IVKVRPRNAEKGTVYQANAVVTPYKLGSSNNAAEASGTRRYAD 72

B933: 7 IVKVRPRNAEKGTVYQANAVVTPYKLGSSNNAAEASGTRRYAD 72

C933: 7 IVKVRPRNAEKGTVYQANAVVTPYKLGSSNNAAEASGTRRYAD 72

D933: 7 IVKVRPRNAEKGTVYQANAVVTPYKLGSSNNAAEASGTRRYAD 72

E933: 7 IVKVRPRNAEKGTVYQANAVVTPYKLGSSNNAAEASGTRRYAD 72

F933: 7 IVKVRPRNAEKGTVYQANAVVTPYKLGSSNNAAEASGTRRYAD 72

G933: 7 IVKVRPRNAEKGTVYQANAVVTPYKLGSSNNAAEASGTRRYAD 72

H933: 7 IVKVRPRNAEKGTVYQANAVVTPYKLGSSNNAAEASGTRRYAD 72

I933: 7 IVKVRPRNAEKGTVYQANAVVTPYKLGSSNNAAEASGTRRYAD 72

J933: 7 IVKVRPRNAEKGTVYQANAVVTPYKLGSSNNAAEASGTRRYAD 72

K933: 7 IVKVRPRNAEKGTVYQANAVVTPYKLGSSNNAAEASGTRRYAD 72

L933: 7 IVKVRPRNAEKGTVYQANAVVTPYKLGSSNNAAEASGTRRYAD 72

M933: 7 IVKVRPRNAEKGTVYQANAVVTPYKLGSSNNAAEASGTRRYAD 72

N933: 7 IVKVRPRNAEKGTVYQANAVVTPYKLGSSNNAAEASGTRRYAD 72

O933: 7 IVKVRPRNAEKGTVYQANAVVTPYKLGSSNNAAEASGTRRYAD 72

P933: 7 IVKVRPRNAEKGTVYQANAVVTPYKLGSSNNAAEASGTRRYAD 72

Q933: 7 IVKVRPRNAEKGTVYQANAVVTPYKLGSSNNAAEASGTRRYAD 72

R933: 7 IVKVRPRNAEKGTVYQANAVVTPYKLGSSNNAAEASGTRRYAD 72

S933: 7 IVKVRPRNAEKGTVYQANAVVTPYKLGSSNNAAEASGTRRYAD 72

T933: 7 IVKVRPRNAEKGTVYQANAVVTPYKLGSSNNAAEASGTRRYAD 72

U933: 7 IVKVRPRNAEKGTVYQANAVVTPYKLGSSNNAAEASGTRRYAD 72

V933: 7 IVKVRPRNAEKGTVYQANAVVTPYKLGSSNNAAEASGTRRYAD 72

W933: 7 IVKVRPRNAEKGTVYQANAVVTPYKLGSSNNAAEASGTRRYAD 72

X933: 7 IVKVRPRNAEKGTVYQANAVVTPYKLGSSNNAAEASGTRRYAD 72

Y933: 7 IVKVRPRNAEKGTVYQANAVVTPYKLGSSNNAAEASGTRRYAD 72

Z933: 7 IVKVRPRNAEKGTVYQANAVVTPYKLGSSNNAAEASGTRRYAD 72

A933: 7 IVKVRPRNAEKGTVYQANAVVTPYKLGSSNNAAEASGTRRYAD 72

B933: 7 IVKVRPRNAEKGTVYQANAVVTPYKLGSSNNAAEASGTRRYAD 72

C933: 7 IVKVRPRNAEKGTVYQANAVVTPYKLGSSNNAAEASGTRRYAD 72

D933: 7 IVKVRPRNAEKGTVYQANAVVTPYKLGSSNNAAEASGTRRYAD 72

E933: 7 IVKVRPRNAEKGTVYQANAVVTPYKLGSSNNAAEASGTRRYAD 72

F933: 7 IVKVRPRNAEKGTVYQANAVVTPYKLGSSNNAAEASGTRRYAD 72

G933: 7 IVKVRPRNAEKGTVYQANAVVTPYKLGSSNNAAEASGTRRYAD 72

H933: 7 IVKVRPRNAEKGTVYQANAVVTPYKLGSSNNAAEASGTRRYAD 72

I933: 7 IVKVRPRNAEKGTVYQANAVVTPYKLGSSNNAAEASGTRRYAD 72

J933: 7 IVKVRPRNAEKGTVYQANAVVTPYKLGSSNNAAEASGTRRYAD 72

K933: 7 IVKVRPRNAEKGTVYQANAVVTPYKLGSSNNAAEASGTRRYAD 72

L933: 7 IVKVRPRNAEKGTVYQANAVVTPYKLGSSNNAAEASGTRRYAD 72

M933: 7 IVKVRPRNAEKGTVYQANAVVTPYKLGSSNNAAEASGTRRYAD 72

N933: 7 IVKVRPRNAEKGTVYQANAVVTPYKLGSSNNAAEASGTRRYAD 72

O933: 7 IVKVRPRNAEKGTVYQANAVVTPYKLGSSNNAAEASGTRRYAD 72

P933: 7 IVKVRPRNAEKGTVYQANAVVTPYKLGSSNNAAEASGTRRYAD 72

Q933: 7 IVKVRPRNAEKGTVYQANAVVTPYKLGSSNNAAEASGTRRYAD 72

R933: 7 IVKVRPRNAEKGTVYQANAVVTPYKLGSSNNAAEASGTRRYAD 72

S933: 7 IVKVRPRNAEKGTVYQANAVVTPYKLGSSNNAAEASGTRRYAD 72

T933: 7 IVKVRPRNAEKGTVYQANAVVTPYKLGSSNNAAEASGTRRYAD 72

U933: 7 IVKVRPRNAEKGTVYQANAVVTPYKLGSSNNAAEASGTRRYAD 72

V933: 7 IVKVRPRNAEKGTVYQANAVVTPYKLGSSNNAAEASGTRRYAD 72

W933: 7 IVKVRPRNAEKGTVYQANAVVTPYKLGSSNNAAEASGTRRYAD 72

X933: 7 IVKVRPRNAEKGTVYQANAVVTPYKLGSSNNAAEASGTRRYAD 72

Y933: 7 IVKVRPRNAEKGTVYQANAVVTPYKLGSSNNAAEASGTRRYAD 72

Z933: 7 IVKVRPRNAEKGTVYQANAVVTPYKLGSSNNAAEASGTRRYAD 72

A933: 7 IVKVRPRNAEKGTVYQANAVVTPYKLGSSNNAAEASGTRRYAD 72

B933: 7 IVKVRPRNAEKGTVYQANAVVTPYKLGSSNNAAEASGTRRYAD 72

C933: 7 IVKVRPRNAEKGTVYQANAVVTPYKLGSSNNAAEASGTRRYAD 72

D933: 7 IVKVRPRNAEKGTVYQANAVVTPYKLGSSNNAAEASGTRRYAD 72

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H933: 7 IVKVRPRNAEKGTVYQANAVVTPYKLGSSNNAAEASGTRRYAD 72

I933: 7 IVKVRPRNAEKGTVYQANAVVTPYKLGSSNNAAEASGTRRYAD 72

J933: 7 IVKVRPRNAEKGTVYQANAVVTPYKLGSSNNAAEASGTRRYAD 72

K933: 7 IVKVRPRNAEKGTVYQANAVVTPYKLGSSNNAAEASGTRRYAD 72

L933: 7 IVKVRPRNAEKGTVYQANAVVTPYKLGSSNNAAEASGTRRYAD 72

M933: 7 IVKVRPRNAEKGTVYQANAVVTPYKLGSSNNAAEASGTRRYAD 72

N933: 7 IVKVRPRNAEKGTVYQANAVVTPYKLGSSNNAAEASGTRRYAD 72

O933: 7 IVKVRPRNAEKGTVYQANAVVTPYKLGSSNNAAEASGTRRYAD 72

P933: 7 IVKVRPRNAEKGTVYQANAVVTPYKLGSSNNAAEASGTRRYAD 72

Q933: 7 IVKVRPRNAEKGTVYQANAVVTPYKLGSSNNAAEASGTRRYAD 72

R933: 7 IVKVRPRNAEKGTVYQANAVVTPYKLGSSNNAAEASGTRRYAD 72

S933: 7 IVKVRPRNAEKGTVYQANAVVTPYKLGSSNNAAEASGTRRYAD 72

T933: 7 IVKVRPRNAEKGTVYQANAVVTPYKLGSSNNAAEASGTRRYAD 72

U933: 7 IVKVRPRNAEKGTVYQANAVVTPYKLGSSNNAAEASGTRRYAD 72

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X933: 7 IVKVRPRNAEKGTVYQANAVVTPYKLGSSNNAAEASGTRRYAD 72

Y933: 7 IVKVRPRNAEKGTVYQANAVVTPYKLGSSNNAAEASGTRRYAD 72

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A933: 7 IVKVRPRNAEKGTVYQANAVVTPYKLGSSNNAAEASGTRRYAD 72

B933: 7 IVKVRPRNAEKGTVYQANAVVTPYKLGSSNNAAEASGTRRYAD 72

C933: 7 IVKVRPRNAEKGTVYQANAVVTPYKLGSSNNAAEASGTRRYAD 72

D933: 7 IVKVRPRNAEKGTVYQANAVVTPYKLGSSNNAAEASGTRRYAD 72

E933: 7 IVKVRPRNAEKGTVYQANAVVTPYKLGSSNNAAEASGTRRYAD 72

F933: 7 IVKVRPRNAEKGTVYQANAVVTPYKLGSSNNAAEASGTRRYAD 72

G933: 7 IVKVRPRNAEKGTVYQANAVVTPYKLGSSNNAAEASGTRRYAD 72

H933: 7 IVKVRPRNAEKGTVYQANAVVTPYKLGSSNNAAEASGTRRYAD 72

I933: 7 IVKVRPRNAEKGTVYQANAVVTPYKLGSSNNAAEASGTRRYAD 72

J933: 7 IVKVRPRNAEKGTVYQANAVVTPYKLGSSNNAAEASGTRRYAD 72

K933: 7 IVKVRPRNAEKGTVYQANAVVTPYKLGSSNNAAEASGTRRYAD 72

L933: 7 IVKVRPRNAEKGTVYQANAVVTPYKLGSSNNAAEASGTRRYAD 72

M933: 7 IVKVRPRNAEKGTVYQANAVVTPYKLGSSNNAAEASGTRRYAD 72

N933: 7 IVKVRPRNAEKGTVYQANAVVTPYKLGSSNNAAEASGTRRYAD 72

O933: 7 IVKVRPRNAEKGTVYQANAVVTPYKLGSSNNAAEASGTRRYAD 72

P933: 7 IVKVRPRNAEKGTVYQANAVVTPYKLGSSNNAAEASGTRRYAD 72

Q933: 7 IVKVRPRNAEKGTVYQANAVVTPYKLGSSNNAAEASGTRRYAD 72

R933: 7 IVKVRPRNAEKGTVYQANAVVTPYKLGSSNNAAEASGTRRYAD 72

S933: 7 IVKVRPRNAEKGTVYQANAVVTPYKLGSSNNAAEASGTRRYAD 72

T933: 7 IVKVRPRNAEKGTVYQANAVVTPYKLGSSNNAAEASGTRRYAD 72

U933: 7 IVKVRPRNAEKGTVYQANAVVTPYKLGSSNNAAEASGTRRYAD 72

V933: 7 IVKVRPR

193	KGYRGGEVYDVYDREHPSROFLEG - QRLVEVGSDDVVYLIBIGCYRHTASTKMDNR	251
171	-SNKG --- NL - KVREHPSGTVYEDLAKXN - VRSQFTELNQDEGNKARTVAYINNMET	223
252	SSSHAIMMLLREERTMTKSGTAKXSRNVLQDASERVAQSOVEQKERT 311	
224	SSSHAVFTLTQW --- HDETMDETEKATISLVDLGERATSTGATGARLKGKA	279
312	HINLSLTIGRTVYDADMATIKGAKAQSYAPRDSKLTTFLDLSGNSKFMATVSP	371
280	EINRSLSTGRTVYIAADMSS - GQRKNNOLVPSRQVSLTUDLSGNSMTAIAISP	338
372	SALNTETLSTLRTYASARDIVYAYQNYNDPARIKRELEPOMEDNR	418
339	EINRSLSTGRTVYIAADMSS - GQRKNNOLVPSRQVSLTUDLSGNSMTAIAISP	405

SOLT 2
 R5735 standard; protein: 955 AA.
 R5735;
 08-MAR-1995 (first entry)
 K39 polypeptide of *Leishmania chagasi*,
 parasite; leishmaniasis; infection; repeat unit; vaccine; antigen;
Leishmania chagasi.
 NO941631-A.
 21-JUL-1994.
 15-JAN-1993; U00324.
 15-JAN-1994; U00324.
 15-JAN-1993; US-00656.
 (IASY-) TASYS CORP.
 Reed SC.
 WPI; 94-249402/30.
 N-PSDB; Q70152.
 Diagnosis of leishmaniasis - by determining the presence of
 antibodies that bind to a K39 repeat unit antigen
 disclosure; Page 12-15; 28PB; English.
 The K39 polypeptide comprises a number of repeated units (described
 in R5735). Detection of antibodies directed against this repeated
 unit in a patients sample is indicative of leishmaniasis. The
 antigenic repeat unit can itself be used as a vaccine to protect
 against infection by a *leishmania* parasite.

PN W0913061-A1.
 PD 18-MAR-1999.
 PF 10-SEP-1998; U19231.
 PR 11-SEP-1997; US-058645.
 PA (REIGC.) UNIT, CALIFORNIA.
 PI Cleveland DM, Goldstein LSB, Sakowicz R, Wood KN;
 WPI; 99/202/33/19.
 DR N-PSDbs; X26819.

PT Centromere-associated protein-E and related nucleic acid
 PS Claim 5; Page 66-67; 77P; English.
 CC The present sequence represents CENP-E (centromere-associated protein-E of Xenopus). The protein has at least one of plus end-directed microtubule motor activity. ATPase (adenosine triphosphatase) activity and microtubule binding activity. CENP-E is the motor that powers chromosome movement toward microtubule plus ends and is essential for congression of chromosomes during mitosis. Modulators of CENP-E can thus control cell proliferation. Agents that modulate CENP-E activity are lead therapeutic, biocultural and diagnostic agents, e.g. for treatment of unwanted cell proliferation (typical of many examples are tumors and metastases; vascular malfunction; inflammatory and immune diseases; angiogenesis; hypertension; restenosis; and fungal infections), also as plant protection agents (selective herbicides, fungicides and insecticides) and plant growth regulators or activators for improving yields. CENP-E is also a diagnostic marker for dividing cells, including CENP-E.

Query Match	14.6%	Score 791;	DB 15;	Length 2954;
Best Local Matches	39.9%	Pred. No. 2,36e-53;		
Local Matches	132;	Mismatches 90;	Indels 17;	Gaps 13
Conservative	92;			
Db	4.3	KSF-NFDRYENHSTSQYBIAVPIRSLAQYNTIAYQTSQSSKGTYMMGTPNSL 101		
Qy	66	RSTWPKDKNAPYQARQEDFQDGLYPLDNLNFQKYNNCIPAYQTSQSGSYSMMGKHK 125		
Db	102	GTPQAIKEVQKIIOP-NREFL--LRFVSYTNEYVTDQDLCDRRKPLIEIRDFR 158		
Qy	126	GVPIRQCDMFRINELQDKKLTCITVEYSLTEYNEYRVDL-NPSTGNLKVREHHSST 184		
Db	159	NVTYADLTELBYVNPBEPVIIQWIKKGERNRHHGETKMKNDHSRSRHTIFRIVESRDRNPT 218		
Qy	185	GPTVEDLAKLIVRSQFQENLMDKBNARTAYAINTNMETTSRHAFTUTL-TOKHDE- 242		
Db	219	NSENCGDAGWMSHLNUVLDLAGSERASOTGAGVPLKGCGNINNSLFLGOV-KKLSD --- 275		
Qy	243	ETRM-DTE-KVAKISVLDLAGSERASTGTAKLKEAGAENSLSITGRVIAALADMSS 300		
Db	276	G-OA-GFGINTYDOSKTRULIONSLGAGNATKTYCTICP--VSPDTEYLSTLQFASAKHR 331		
Qy	301	GIKOKKQKLYPDSVLTWLDLGNSMTMIAIAISPADINEEFTLSTLRYADSASKR 360		
Db	332	NTPHVNVEVDDEALLKRYKKEELDKKOLEN 362		
Qy	361	NHAYVNEED-PNARMTRLEKELAQRISKLSQ 390		

PN	W0991306.1-Al.
PD	18 Mar 1999
PF	10-SSP-1998; U19231.
PR	11-SSP-1997; US-058645.
CC	Xenopus. The protein has at least one of plus end-directed microtubule motor activity. AtPase (adenosine triphosphatase) activity and microtubule binding activity. CENP-E is the motor that powers chromosome movement toward microtubule plus ends and is essential for congression of chromosomes during mitosis. Modulators of CENP-E can thus control cell proliferation. Agents that modulate CENP-E activity are lead therapeutic, biogultural and diagnostic agents, e.g. for treatment of unwanted cell proliferation (typical of many examples are tumors and metastases; vascular malfunction, inflammatory and immune diseases; angiogenesis; hypertension; restenosis; and fungal infections), also as plant-protective agents (selective herbicides, fungicides and insecticides) and plant growth regulators or activators for improving yields. CENP-E is also a diagnostic marker for dividing cells, including cancer cells.
DR	DR 8619.
DR	DR 99-229233-19.
PT	Centromere-associated protein-E and related nucleic acid
PS	Claim 5; Page 66-67; 7TP; English
CC	The present sequence represents CENP-E (centromere-associated protein-E of Xenopus. The protein has at least one of plus end-directed microtubule motor activity. AtPase (adenosine triphosphatase) activity and microtubule binding activity. CENP-E is the motor that powers chromosome movement toward microtubule plus ends and is essential for congression of chromosomes during mitosis. Modulators of CENP-E can thus control cell proliferation. Agents that modulate CENP-E activity are lead therapeutic, biogultural and diagnostic agents, e.g. for treatment of unwanted cell proliferation (typical of many examples are tumors and metastases; vascular malfunction, inflammatory and immune diseases; angiogenesis; hypertension; restenosis; and fungal infections), also as plant-protective agents (selective herbicides, fungicides and insecticides) and plant growth regulators or activators for improving yields. CENP-E is also a diagnostic marker for dividing cells, including cancer cells.
Sq	Sequence 2954 AA;
Query Match	14.6%; Score 791; DB 1; Length 2954;
Best Local Similarity	39.9%; Pred. No. 2.3e-53;
Matches	132; Conservative 92; Mismatches 90; Indels 17; Gaps 13
Db	43 KSP-NFDYENHSQTSQYQIAPIVSLAQCGNTTAYGOTSGKTYTMGTPNS 101
Qy	66 RSWSTDKNAPNYAQARQEDFQDLSPLDNFKYNNCIPAYGOTSGSNSYMGKREH 125
Db	102 GIPQAIQEVFKIQEIP-NREFL-LAVSMEYIINETVQDLCDRRKPKLEIRDFFNR 158
Qy	126 GIVPRICODPRKINLQDQKILCUTVSEVSTLEYNVRDLD-NPSTGKNUKVBPBOST 184
Db	159 NTVVADITEEYVNPHEVYIWKIGKRNHRHGETKANDHSRSRHTIFRIVESRDRNDEP 218
Qy	185 GPTVDEKLAKVYRSQFQEJENLMDEGNSKARTVAAHNMEETSSRSHAVYTFD 242
Db	219 NSNCDCGAYMWSHLNIVDLAGSERASRGTGAGSYVLKGGCINNSLILQCVKKLSD-- 275
Qy	243 ETM-DTE-KVAKISLVDLAESEATSTGAGKLKGAEINSLSTLRVIAAADDSS 300
Db	276 G-QA-GFFINYDRSKUTRILQNSLGNAKTVIICPT--VSFDLSTLQFASAKHIVR 331
Qy	301 GRKRNQQLPYRDSTLWNLKDSLGSNSMTMAMIAISPADINEEFTSLRIVADSKRKK 360
Db	332 NTHVNEVLDDEALAKRYKELDIKKKOLE 362
Qy	361 NHAVVND-PNARMIRELKEELAQRSLKQS 390

Query Match	Score 707;	DB 1; Length 411;	
Best Local Similarity	42.3%	Pred. No. 2,48e-46;	
Matches	138; Conservative	Mismatches 91; Indels 20; Gaps 12;	
Db	55 FDVKFPPNASEQKTYNEAKSLSVVDLQAGNYCTFAYGTSQGKTHMEGVIGDSVKGIGI 114		
Qy	71 FDKNPNTARYDQDFDQLGPVLPNQKGNICIAFGQGSKCSYSMG-GKE-GIV 127		
Db	115 IPRIVDIDFNHYAM-EVNLEDFKIVSTYMDKTRDOLDS-KYVNLSHEDRNRYV 171		
Qy	128 IPRICDMFRINFLQDKNQTCIV EYSTELEYNTRDILPSKGNLKVHRHSTGPY 187		
Db	172 VKGATREVSSPDEVIEEGKSKRNLQKTRAVTMNEHSRSHEVFLINKVKGNLNOKKL- 230		
Qy	188 VEDLAKLVYRSPQIENLDEGNKNAKRVIAHNTNETSSBRAVFTLTQKWHDETMQ 247		
Db	231 S--GFLYDOLGSKESVKSKGARGSTYDDEANINKSALGNVLSALAD--GN--KTH 262		
Qy	248 TEVAKISLVLQDAGSERATSTGAYGARLREGELNRLSLGTRVIAALMSSGQRKRNQ 307		
Db	283 -IYPROSKTRIQLQESIGGNNATVIVCSPASNESETISLDFGRATVYVCNE 341		
Qy	308 LVPYROSUTNLQDGGSNNTAMIAASPADINFEETLSTLRYADSAKRNHAYVNE 367		
Db	342 ELTAEEWKRRTREKEKKNARLKGKVE 367		
Qy	368 D-PNARMR-EL-KEEALQRSLQ 389		

RESULT	5	standard; protein; 411 AA.	
ID	W72744	AC W72744.	
DT	11-JAN-1995 (first entry)	DE Drosophila kinesin N-terminal 411 amino acid residues.	KW Drosophila; kinesin; separation; hybridisation; target site; complex mixture; motor protein; actively transported; separated; KW microtubule; motor protein; actively transported; separated; KW microtubule.
OS Drosophila sp.	PS D53856597A.	PN PD 03-NOV-1998.	CA 13-SEP-1996; US-713815.
PT	03-NOV-1998; 713815.	PR 13-SEP-1996; US-713815.	DT (UTAH) UNIV UTAH RES FOUND.
PA (UTAH) UNIV UTAH RES FOUND.	PI Stewart RJ.	PA (UTAH) UNIV UTAH RES FOUND.	PR 98-609236/51.
CC	PT Separation of selected molecules, e.g. DNA, from complex mixtures - uses specific apparatus to allow the selected molecule to bind to motor proteins, and be actively transported and separated away along micro-tubules.	PT Separation of selected molecules, e.g. DNA, from complex mixtures - uses specific apparatus to allow the selected molecule to bind to motor proteins, and be actively transported and separated away along micro-tubules.	CC A method has been developed of separating selected molecule from a mixture of molecules. The method comprises: (a) a separation device comprising a loading reservoir and a receiving reservoir coupled by a channel with microtubules immobilised on its surface and aligned parallel to a longitudinal axis of the channel; (b) loading the loading reservoir with an aqueous solution of the mixture of molecules; (c) adding a motor-ligand composition and ATP to the solution, where the motor-ligand comprises, (i) a processive motor capable of attaching to the immobilised microtubules, and moving in the presence of ATP as a source of chemical energy, and (ii) a ligand coupled to the motor protein, where the ligand is capable of binding the selected molecule, so that the ligand binds the selected molecule and the motor protein attaches to the immobilised microtubules and transports the bound selected molecules along the microtubules and transports the selected molecule from the receiving reservoir; and (d) removing the selected molecule from the receiving reservoir. The method and the system are used for the separation of specific molecules from complex mixtures. The molecules to be separated (e.g. DNA) binds to the motor protein due to the presence of the specific binding ligands. Activation of these enables them to travel down a preformed channel in a specially made piece of apparatus. They can then be removed easily without contaminants of other mixture particles. The present sequence represents the N-terminal 411 amino acid residues of Drosophila kinesin for use in the method of the invention.
CC	CC Claim 3: Column 25-28: 240P; English.	CC Claim 3, column 23-26: 240P; English.	CC A method has been developed of separating selected molecule from a mixture of molecules. The method comprises: (a) a separation device comprising a loading reservoir and a receiving reservoir coupled by a channel with microtubules immobilised on its surface and aligned parallel to a longitudinal axis of the channel; (b) loading the loading reservoir with an aqueous solution of the mixture of molecules; (c) adding a motor-ligand composition and ATP to the solution, where the motor-ligand comprises, (i) a processive motor capable of attaching to the immobilised microtubules, and moving in the presence of ATP as a source of chemical energy, and (ii) a ligand coupled to the motor protein, where the ligand is capable of binding the selected molecule, so that the ligand binds the selected molecule and the motor protein attaches to the immobilised microtubules and transports the bound selected molecules along the microtubules and transports the selected molecule from the receiving reservoir; and (d) removing the selected molecule from the receiving reservoir. The method and the system are used for the separation of specific molecules from complex mixtures. The molecules to be separated (e.g. DNA) binds to the motor protein due to the presence of the specific binding ligands. Activation of these enables them to travel down a preformed channel in a specially made piece of apparatus. They can then be removed easily without contaminants of other mixture particles. The present sequence represents the N-terminal 411 amino acid residues of Drosophila kinesin for use in the method of the invention.
CC	CC Sequence 411 AA;	CC Sequence 411 AA;	CC
CC	CC Query Match 13.0%; Score 707; DB 1; Length 411;	CC Query Match 13.0%; Score 707; DB 1; Length 411;	CC
CC	CC Best Local Similarity 42.3%; Pred. No. 2,48e-46;	CC Best Local Similarity 42.3%; Pred. No. 2,48e-46;	CC
CC	CC Matches 138; Conservative 77; Mismatches 91; Indels 20; Gaps 12;	CC Matches 138; Conservative 77; Mismatches 91; Indels 20; Gaps 12;	CC
Db	55 FDVKFPPNASEQKTYNEAKSLSVVDLQAGNYCTFAYGTSQGKTHMEGVIGDSVKGIGI 114	Db 55 FDVKFPPNASEQKTYNEAKSLSVVDLQAGNYCTFAYGTSQGKTHMEGVIGDSVKGIGI 114	Db 55 FDVKFPPNASEQKTYNEAKSLSVVDLQAGNYCTFAYGTSQGKTHMEGVIGDSVKGIGI 114
Qy	71 FDKNPNTARYDQDFDQLGPVLPNQKGNICIAFGQGSKCSYSMG-GKE-GIV 127	Qy 71 FDKNPNTARYDQDFDQLGPVLPNQKGNICIAFGQGSKCSYSMG-GKE-GIV 127	Qy 71 FDKNPNTARYDQDFDQLGPVLPNQKGNICIAFGQGSKCSYSMG-GKE-GIV 127
Db	115 IPRIVDIDFNHYAM-EVNLEDFKIVSTYMDKTRDOLDS-KYVNLSHEDRNRYV 171	Db 115 IPRIVDIDFNHYAM-EVNLEDFKIVSTYMDKTRDOLDS-KYVNLSHEDRNRYV 171	Db 115 IPRIVDIDFNHYAM-EVNLEDFKIVSTYMDKTRDOLDS-KYVNLSHEDRNRYV 171
Qy	128 IPRICDMFRINFLQDKNQTCIV EYSTELEYNTRDILPSKGNLKVHRHSTGPY 187	Qy 128 IPRICDMFRINFLQDKNQTCIV EYSTELEYNTRDILPSKGNLKVHRHSTGPY 187	Qy 128 IPRICDMFRINFLQDKNQTCIV EYSTELEYNTRDILPSKGNLKVHRHSTGPY 187
Db	172 VKGATREVSSPDEVIEEGKSKRNLQKTRAVTMNEHSRSHEVFLINKVKGNLNOKKL- 230	Db 172 VKGATREVSSPDEVIEEGKSKRNLQKTRAVTMNEHSRSHEVFLINKVKGNLNOKKL- 230	Db 172 VKGATREVSSPDEVIEEGKSKRNLQKTRAVTMNEHSRSHEVFLINKVKGNLNOKKL- 230
Qy	188 VEDLAKLVYRSPQIENLDEGNKNAKRVIAHNTNETSSBRAVFTLTQKWHDETMQ 247	Qy 188 VEDLAKLVYRSPQIENLDEGNKNAKRVIAHNTNETSSBRAVFTLTQKWHDETMQ 247	Qy 188 VEDLAKLVYRSPQIENLDEGNKNAKRVIAHNTNETSSBRAVFTLTQKWHDETMQ 247
Db	231 S--GFLYDOLGSKESVKSKGARGSTYDDEANINKSALGNVLSALAD--GN--KTH 262	Db 231 S--GFLYDOLGSKESVKSKGARGSTYDDEANINKSALGNVLSALAD--GN--KTH 262	Db 231 S--GFLYDOLGSKESVKSKGARGSTYDDEANINKSALGNVLSALAD--GN--KTH 262
Qy	248 TEVAKISLVLQDAGSERATSTGAYGARLREGELNRLSLGTRVIAALMSSGQRKRNQ 307	Qy 248 TEVAKISLVLQDAGSERATSTGAYGARLREGELNRLSLGTRVIAALMSSGQRKRNQ 307	Qy 248 TEVAKISLVLQDAGSERATSTGAYGARLREGELNRLSLGTRVIAALMSSGQRKRNQ 307
Db	283 -IYPROSKTRIQLQESIGGNNATVIVCSPASNESETISLDFGRATVYVCNE 341	Db 283 -IYPROSKTRIQLQESIGGNNATVIVCSPASNESETISLDFGRATVYVCNE 341	Db 283 -IYPROSKTRIQLQESIGGNNATVIVCSPASNESETISLDFGRATVYVCNE 341
Qy	308 LVPYROSUTNLQDGGSNNTAMIAASPADINFEETLSTLRYADSAKRNHAYVNE 367	Qy 308 LVPYROSUTNLQDGGSNNTAMIAASPADINFEETLSTLRYADSAKRNHAYVNE 367	Qy 308 LVPYROSUTNLQDGGSNNTAMIAASPADINFEETLSTLRYADSAKRNHAYVNE 367
Db	342 ELTAEEWKRRTREKEKKNARLKGKVE 367	Db 342 ELTAEEWKRRTREKEKKNARLKGKVE 367	Db 342 ELTAEEWKRRTREKEKKNARLKGKVE 367
Qy	368 D-PNARMR-EL-KEEALQRSLQ 389	Qy 368 D-PNARMR-EL-KEEALQRSLQ 389	Qy 368 D-PNARMR-EL-KEEALQRSLQ 389

FT	Domain	/note= "ATP-binding P-loop" 424..435	FT	Modified_site	site*	FT	Modified_site	290..292	FT	Modified_site	/note= "potential protein kinase C phosphorylation
FT	Modified_site	/note= "kinase motor domain signature" 9..11	FT	Modified_site	FT	FT	Modified_site	301..303	FT	Modified_site	/note= "potential protein kinase C phosphorylation
FT	Modified_site	/note= "Asn is N-glycosylated" 106..109	FT	Modified_site	FT	FT	Modified_site	344..346	FT	Modified_site	/note= "potential protein kinase C phosphorylation
FT	Modified_site	/note= "Asn is N-glycosylated" 244..247	FT	Modified_site	FT	FT	Modified_site	344..346	FT	Modified_site	/note= "potential protein kinase C phosphorylation
FT	Modified_site	/note= "Asn is N-glycosylated" 455..459	FT	Modified_site	FT	FT	Modified_site	392..394	FT	Modified_site	/note= "potential protein kinase C phosphorylation
FT	Modified_site	/note= "Asn is N-glycosylated" 127..130	FT	Modified_site	FT	FT	Modified_site	405..407	FT	Modified_site	/note= "potential protein kinase C phosphorylation
FT	Modified_site	/note= "potential cAMP- and cAMP-dependent protein kinase phosphorylation site"	FT	Modified_site	FT	FT	Modified_site	516..518	FT	Modified_site	/note= "potential protein kinase C phosphorylation
FT	Modified_site	/note= "potential cAMP- and cAMP-dependent protein kinase phosphorylation site"	FT	Modified_site	FT	FT	Modified_site	516..518	FT	Modified_site	/note= "potential protein kinase C phosphorylation
FT	Modified_site	4..7	FT	Modified_site	/note= "potential casein kinase II phosphorylation site"	FT	Modified_site	608..610	FT	Modified_site	/note= "potential protein kinase C phosphorylation
FT	Modified_site	27..30	FT	Modified_site	/note= "potential casein kinase II phosphorylation site"	FT	Modified_site	656..658	FT	Modified_site	/note= "potential protein kinase C phosphorylation
FT	Modified_site	108..111	FT	Modified_site	/note= "potential casein kinase II phosphorylation site"	FT	Modified_site	670..672	FT	Modified_site	/note= "potential protein kinase C phosphorylation
FT	Modified_site	187..190	FT	Modified_site	/note= "potential casein kinase II phosphorylation site"	FT	Modified_site	673..675	FT	Modified_site	/note= "potential protein kinase C phosphorylation
FT	Modified_site	273..280	FT	Modified_site	/note= "potential casein kinase II phosphorylation site"	FT	Modified_site	676..678	FT	Modified_site	/note= "potential protein kinase C phosphorylation
FT	Modified_site	338..341	FT	Modified_site	/note= "potential casein kinase II phosphorylation site"	FT	Modified_site	679..681	FT	Modified_site	/note= "potential protein kinase C phosphorylation
FT	Modified_site	427..430	FT	Modified_site	/note= "potential casein kinase II phosphorylation site"	FT	Modified_site	682..685	FT	Modified_site	/note= "potential protein kinase C phosphorylation
FT	Modified_site	441..444	FT	Modified_site	/note= "potential casein kinase II phosphorylation site"	FT	Modified_site	686..689	FT	Modified_site	/note= "potential protein kinase C phosphorylation
FT	Modified_site	447..450	FT	Modified_site	/note= "potential casein kinase II phosphorylation site"	FT	Modified_site	690..693	FT	Modified_site	/note= "potential protein kinase C phosphorylation
FT	Modified_site	582..585	FT	Modified_site	/note= "potential casein kinase II phosphorylation site"	FT	Modified_site	694..697	FT	Modified_site	/note= "potential protein kinase C phosphorylation
FT	Modified_site	634..637	FT	Modified_site	/note= "potential casein kinase II phosphorylation site"	FT	Modified_site	698..701	FT	Modified_site	/note= "potential protein kinase C phosphorylation
FT	Modified_site	58..60	FT	Modified_site	/note= "potential protein kinase C phosphorylation site"	FT	Modified_site	702..705	FT	Modified_site	/note= "potential protein kinase C phosphorylation
-	Modified_site	233..241	FT	Modified_site	/note= "potential tyrosine kinase phosphorylation site"	FT	Modified_site	73..75	FT	Modified_site	/note= "potential protein kinase C phosphorylation
FT	Modified_site	329..336	FT	Modified_site	/note= "potential tyrosine kinase phosphorylation site"	FT	Modified_site	88..90	FT	Modified_site	/note= "potential protein kinase C phosphorylation
FT	Modified_site	126..128	FT	Modified_site	/note= "potential protein kinase C phosphorylation site"	FT	Modified_site	126..128	FT	Modified_site	/note= "potential protein kinase C phosphorylation
FT	Modified_site	246..248	FT	Modified_site	/note= "potential protein kinase C phosphorylation site"	FT	Modified_site	266..268	FT	Modified_site	/note= "potential protein kinase C phosphorylation

Score 424; DB 1; Length 679;

Best Local Similarity 35.7%; Pred. No. 4..74e-23; Indels 39; Gaps 23;

Matches 133; Conservative 80; Mismatches 121; Delins 39; Gaps 23; Sequence 679 AA;

Region	Qualifiers	Location	9
W03035	standard; protein: 1201 AA.	W03035; 1999 (first entry)	W03035; 1999 (first entry)
Drosophila sp.	COS2 protein.	Drosophila sp.; COS2; protein.	Drosophila sp.; COS2; protein.
Cos2; fruitfly; costal; kinetochore-related; hedgehog; modulate; mapping; gene therapy; prophylactic; therapeutic; treatment; cancer; meningioma; basal cell carcinoma; glioma; medulloblastoma; breast carcinoma; hedgehog signalling pathway; infestation; treatment; contraception; developmental abnormalities; immunogen.			
Drosophila sp.			
Key	Location/Qualifiers		
Region	1_450	9	W03035 standard; protein: 1201 AA.
Binding_site	174..181	note="N-terminal region"	
Binding_site	237..239	note="Putative nucleotide binding motif N1 (P-loop)"	
Binding_site	265..269	note="Putative microtubule binding motif N"	
Binding_site	298..303	note="Putative nucleotide binding motif N2"	
Binding_site	340..345	note="Putative nucleotide binding motif N3"	
Region	643..990	note="Putative microtubule binding motif N"	
Region	643..650	note="central region"	
Region	651..656	note="heptad repeat"	
Region	657..663	note="heptad repeat"	
Region	664..670	note="heptad repeat"	
Region	671..677	note="heptad repeat"	
Region	678..684	note="heptad repeat"	
Region	685..691	note="heptad repeat"	
Region	692..698	note="heptad repeat"	
Region	706..712	note="heptad repeat"	

FT	Region	713 . 719	"note" "heptad repeat"
FT	Region	720 . 726	"note" "heptad repeat"
FT	Region	727 . 733	"note" "heptad repeat"
FT	Region	740 . 746	"note" "heptad repeat"
FT	Region	747 . 753	"note" "heptad repeat"
FT	Region	754 . 760	"note" "heptad repeat"
FT	Region	761 . 767	"note" "heptad repeat"
FT	Region	771 . 777	"note" "heptad repeat"
FT	Region	778 . 784	"note" "heptad repeat"
FT	Region	785 . 791	"note" "heptad repeat"
FT	Region	792 . 798	"note" "heptad repeat"
FT	Region	799 . 805	"note" "heptad repeat"
FT	Region	806 . 812	"note" "heptad repeat"
FT	Region	833 . 839	"note" "heptad repeat"
FT	Region	840 . 846	"note" "heptad repeat"
FT	Region	847 . 853	"note" "heptad repeat"
FT	Misc_difference	857	"note" "heptad repeat"
FT	Region	870 . 876	"label" unknown
FT	Region	877 . 883	"note" "heptad repeat"
FT	Region	884 . 890	"note" "heptad repeat"
FT	Region	905 . 911	"note" "heptad repeat"
FT	Region	912 . 918	"note" "heptad repeat"
FT	Region	919 . 925	"note" "heptad repeat"
FT	Region	926 . 932	"note" "heptad repeat"
FT	Region	963 . 969	"note" "heptad repeat"
FT	Region	970 . 976	"note" "heptad repeat"
FT	Region	977 . 983	"note" "heptad repeat"
FT	Region	984 . 990	"note" "heptad repeat"
FT	Region	1050 . 1056	"note" "heptad repeat"
FT			"note" "C-terminal reg"
PN		W0990403-A1	
PD		07-JAN-1999	
PD		18-JUN-1998; 012820	
PR		30-JUN-1997; US-051347	
(STRD)	UNIV LELAND STANFORD JUNIOR		
PI	SCOTT MP, SISSON JC;		
DR	WPI: 99-0990403-008.		
N-SPD	DR-N-SPD: V72291		
PR	New-costal1 (cos2) gene - used to iden		
PT	proteins		
PT	Claim 3; Page 31-34; 42pp; English.		
PS	This sequence represents a Cos2 gene in		
CC	Costal2 protein (also known as the Costal		
CC	protein that accumulates preferentially		
CC	in the hedgehog this sequence is used to de-		

CC In producing compositions that modulate the expression or function of the encoded protein, for gene therapy, mapping functional regions of the protein and in studying associated physiological pathways. In addition, the modulation of Cox 2 gene activity is used for prophylactic and therapeutic purposes such as treatment of cancers (e.g. basal cell carcinoma, glioma, medulloblastoma, meningioma, breast carcinoma, meningitis, pathway function, identification of cell type based on expression, infertility treatment, contraception, developmental abnormalities. The encoded protein is useful for producing specific antibodies. In some sequences for biologically active agents that modulate Cox 2 function and that act in the hedgehog signalling pathway. The protein can also be used for therapeutic and prophylactic purposes. Sequence 1201 AA;

Query Match Score 211; DB 1; Length 1201;
Best Local Similarity 31.6%; Pred. No. 2.10e-16; 7;

Matches 50; Conservative 42; Mismatches 56; Indels 10; Gaps 7;

Db 268 AHTLFITLEQDQYSKEGLIQQ-HRLSTASPSDLCGTCRCCDQ-PPGRLP-D-A---GLC 319

Qy 227 SHAVFLTITQKWHDEETMDTKEVAKISVNDLAGRSATSGAAGLAKEGAEINRALS 266

Db 320 MLEQVISTLTD-POLQVYNGNTGQVTLPLKDSFGERQTVLIVCSPLEHLPET 378

Qy 287 TLRVTFARIAADSSGCRKRNQVLPVYPROSTVTLKLDSGNGNTMATAISPADNFET 346

Db 379 IGLNQPAFKVQCVRNQVINTYSDDINMIVPAEPVPE 416

Qy 347 LSTLTYADSARKRKHAVVNE-DPANMRTRKEELAQ 383

RESULT 10
ID W2094 standard; Protein: 1612 AA.

AC W2094_1; 20-Nov-1997 (first entry)

DE Ras-binding protein p180.

KW Inhibit: tumour formation; p180; modified AF-6; recombinant production;

KW Inhibit: tumour formation; metastasis; screen.

OS Homo sapiens.

PN 3039189704.

PD 29-JUL-1997.

PP 07-DEC-1995; 31102381.

PR 15-Nov-1995; JP-2/97109.

PA (KIRI) KIRIN BREWERY KK.

DR WPI; 97-42979/10.

DR N-PSDB; T85642.

PT Active type Ras-binding protein p180 - used to inhibit tumour

PT formation

PS Claim 1; Page 11-17; 24pp; Japanese.

CC This sequence is a protein, p180, which comprises a modified AF-6 amino acid sequence which has active Ras-binding activity. Host cells transformed with the cDNA can be cultured for the recombinant production of p180. p180 inhibits tumour formation or metastasis. It can also be used to screen for substances that inhibit binding between active type

CC Ras protein and AF-6.

Sequence 1612 AA;

Query Match Score 196; DB 1; Length 1612;
Best Local Similarity 34.5%; Pred. No. 2.67e-05; 4;

Matches 38; Conservative 24; Mismatches 44; Indels 4; Gaps 4;

Db 383 LPLVLESPDGS-DSRDKPVLKPLS-SYVTEGVKEKDDNS-TOLFGPGIOPHCDLTNNDG 441

Qy 493 MHPVNLNSDDPLLA-B-CLAYVNPGLQTRVGNVNDVQASHEVKEVYDPSQDA 550

Db 442 WVVTRSRNSDDETFEGORISSETMLOSGMKYVCGASHEVKEVYDPSQDA 491

Qy 551 WVVTPNEKAAMV-VNGVDRKPKPLRSLGRTLDFPFRNHPPEAR 599

RESULT 11
ID R66457 standard; Protein: 1612 AA.

AC R66457;

CC In producing compositions that modulate the expression or function of the encoded protein, for gene therapy, mapping functional regions of the protein; acute lymphoblastic leukaemia; acute nonlymphoblastic leukaemia; chromosomal translocation; abnormality; detection; CC chimeric AF-1/AF-6 protein.

CC Homo sapiens.

PN W0426910-A.

PD 24-NOV-1994.

PP 24-APR-1994; U04496.

PR 14-MAY-1993; US-052443.

PA (UJJE) UNIV JEFFERSON THOMAS.

PI Canadia E. Troeze C;

DR WPI; 95-06818/01.

PT New acute lymphocytic leukaemia gene prods. - used for the

PT diagnosis and treatment of leukaemias, partic. acute

PT lymphoblastic or nonlymphoblastic leukaemia.

CC Monoclonal antibodies which bind to at least part of the chimeric

CC AF-1/AF-6 protein R66456-R66158 are claimed. The antibodies are

CC used for diagnosing acute lymphoblastic and non-lymphoblastic

CC leukaemia.

SQ Sequence 1612 AA;

Query Match Score 196; DB 1; Length 1612;

Best Local Similarity 34.5%; Pred. No. 2.67e-05;

Matches 38; Conservative 24; Mismatches 44; Indels 4; Gaps 4;

Db 383 LPLVLESPDGS-DSRDKPVLKPLS-SYVTEGVKEKDDNS-TOLFGPGIOPHCDLTNNDG 441

Qy 493 MHPVNLNSDDPLLA-B-CLAYVNPGLQTRVGNVNDVQASHEVKEVYDPSQDA 550

Db 442 WVVTRSRNSDDETFEGORISSETMLOSGMKYVCGASHEVKEVYDPSQDA 491

Qy 551 WVVTPNEKAAMV-VNGVDRKPKPLRSLGRTLDFPFRNHPPEAR 599

RESULT 12
ID Y0242 standard; protein; 1829 AA.

AC Y0242; 31-MAR-1996; 307643.

PR 21-SEP-1997; JP-257043.

PA (NISIC) JAPAN SCI & TECHNOLOGY CORP.

PA (ORAI) ORAISHI H.

PA (KADA) WADA M.

DR WPI; 99-206773/18.

PT New normal filiment-binding protein 1-Afadin and its derivatives may have a molecular weight of around 25 kD. 1-Afadin and its derivatives may be used to clarify

CC the mechanisms of infiltration and metastasis of carcinoma useful in

CC diagnosing or treating carcinomas.

SQ Sequence 1829 AA;

Query Match Score 183; DB 1; Length 1829;

Best Local Similarity 35.6%; Pred. No. 2.3e-04;

Matches 37; Conservative 19; Mismatches 37;

Indels 2; Gaps 2;

Db 448 LYPLQSLTVEYCEKEKDDNS-TOLFGPGIOPHCDLTNNDGUTVPSNDAEVYDPSQDA 476

Qy 510 WVVTRSRNSDDETFEGORISSETMLOSGMKYVCGASHEVKEVYDPSQDA 550

Db 442 WVVTRSRNSDDETFEGORISSETMLOSGMKYVCGASHEVKEVYDPSQDA 491

Qy 551 WVVTPNEKAAMV-VNGVDRKPKPLRSLGRTLDFPFRNHPPEAR 599

RESULT 13
ID R66457 standard; Protein: 1612 AA.

AC R66457;

PT

CC

CC

CC

CC

CC

CC

CC

PR	17-JAN-1997; JP-019870.
PA	(KIRI) KIRIN BREWERY KK.
DR	WP1; 98-46010/40.
DR	N-PSDB; V42941.
PT	New protein exhibiting protein kinase activity - is not capable of binding to active Rho protein or its derivative. Used, e.g. therapeutically.
PT	Claim 1; Fig 1; Gopp; Japanese.
PS	The present sequence encodes a protein which exhibits protein kinase activity and is not capable of binding to active Rho protein or its derivative. The materials may be used for the preparation of therapeutic compositions.
SQ	Sequence 1354 AA;
Query Match	2 2%; Score 120; DB 1; Length 1354;
Best Local Similarity	28 1%; Pred. No. 5.12e+00;
Matches	32; Mismatches 66; Indels 7; Gaps 6.
Db	849 EQYFSTL-YKTVKELKEEIEKRENLUKIQELQNEKETLATQOLDLASTKAESBOLARG 907
Qy	344 EETLSTLRYADSAKRIKHNAYVNEDPARNMRELKELQALRKLOSSGGGGGGGGGG 403
Db	908 LLBQYFELTQESKAASRNQEQETDQHVSRLLEANSMLTIDILRE-NEBLTEKM 966
Qy	404 PVEESTPPDTPLEQIVSQDPATVK -RMSKAEIYEQ-LNGS-EKLYRDNQTWEKL 459
RESULT	15
ID	W23654 standard; Protein: 1354 AA.
AC	W23654.
DT	13-OCT-1997 (first entry)
DE	Physiologically active protein p160.
KW	Rho binding activity; protein kinase; protein binding; host cell; recombinant production; human.
OS	Homo sapiens .
PN	J0911563-A.
PD	27-MAY-1997; 184102553.
PR	14-SPB-1995; JP-262553.
PA	(KIRI) KIRIN BREWERY KK.
DR	WP1; 97-3590/31.
DR	N-PSDB; T8203.
PT	Physiological activity active protein p160 - has rho binding activity and protein kinase activity.
CC	The present sequence represents the physiologically active protein p160, which has active Rho protein-binding and protein kinase activities. The nucleotide sequence can be put into a vector which can then be used to transform a host cell. The host cell can be cultured for the recombinant production of the p160 protein. The p160 protein can be used in a method to screen for compounds that inhibit the protein kinase activity.
SQ	Sequence 1354 AA;
Query Match	2 2%; Score 120; DB 1; Length 1354;
Best Local Similarity	28 1%; Pred. No. 5.12e+00;
Matches	32; Mismatches 66; Indels 7; Gaps 6.
Db	849 EQYFSTL-YKTVKELKEEIEKRENLUKIQELQNEKETLATQOLDLASTKAESBOLARG 907
Qy	344 EETLSTLRYADSAKRIKHNAYVNEDPARNMRELKELQALRKLOSSGGGGGGGGGG 403
Db	908 LLBQYFELTQESKAASRNQEQETDQHVSRLLEANSMLTIDILRE-NEBLTEKM 966
Qy	404 PVEESTPPDTPLEQIVSQDPATVK -RMSKAEIYEQ-LNGS-EKLYRDNQTWEKL 459
RESULT	14
ID	W1020 standard; Protein: 1354 AA.
W1020;	27-OCT-1998 (first entry)
PT	A modified Rho target protein kinase p160 protein. Preparation: protein kinase activity; Rho protein; preparation; therapeutic composition.
PS	Homo sapiens .
DR	J10191985-A.
PR	28-JUL-1998; 019870.
PA	AKTEETH-K-EETEAEELGISTEKG 484
DR	AKTEETH-K-EETEAEELGISTEKG 484
PT	Claim 1; Fig 1; Gopp; Japanese.
PS	The present sequence encodes a protein which exhibits protein kinase activity and is not capable of binding to active Rho protein or its derivative. The materials may be used for the preparation of therapeutic compositions.
SQ	Sequence 1354 AA;
Query Match	2 2%; Score 120; DB 1; Length 1354;
Best Local Similarity	28 1%; Pred. No. 5.12e+00;
Matches	32; Mismatches 66; Indels 7; Gaps 6.
Db	849 EQYFSTL-YKTVKELKEEIEKRENLUKIQELQNEKETLATQOLDLASTKAESBOLARG 907
Qy	344 EETLSTLRYADSAKRIKHNAYVNEDPARNMRELKELQALRKLOSSGGGGGGGGGG 403
Db	908 LLBQYFELTQESKAASRNQEQETDQHVSRLLEANSMLTIDILRE-NEBLTEKM 966
Qy	404 PVEESTPPDTPLEQIVSQDPATVK -RMSKAEIYEQ-LNGS-EKLYRDNQTWEKL 459
RESULT	14
ID	W1020 standard; Protein: 1354 AA.
W1020;	27-OCT-1998 (first entry)
PT	A modified Rho target protein kinase p160 protein. Preparation: protein kinase activity; Rho protein; preparation; therapeutic composition.
PS	Homo sapiens .
DR	J10191985-A.
PR	28-JUL-1998; 019870.
PA	AKTEETH-K-EETEAEELGISTEKG 484
DR	AKTEETH-K-EETEAEELGISTEKG 484

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Db	228	KKDPETNLSTEKVSKLISVLQLAGSFERADSTGAKTRLGEGANIKSITLICKVISALAE	287
Qy	238	KVHDETRKMDFEVKAKSLVDLGSERATSIYGARLKGAEINRSLTGRIJAALAD	297
Db	288	VSK*KKKDTIPIYDSEVTLWLRNLLGGSNRTMAMVSPADINDETLSTYRADAK	346
Qy	298	MSSGKKNOLVYPRDSEVTLWLRNLLGGSNRTMAMVSPADINDETLSTYRADAK	357
Db	347	QIKKNAVTEENPNAKLYKREKKEVTRKLQLDRLAAGLQD1-IDTSMGSITSS-PSSCSNS	404
Qy	358	RKHNAYNEENPNAKLYKREKKEVTRKLQLDRLAAGLQD1-IDTSMGSITSS-PSSCSNS	417
Db	405	QVGLDSVTSIQRIMSTPGEAETRKLSEKITAENETWKLAKTEBILMEALLA	464
Oy	418	QI-V-SICQDPAUTPKRNSKAE-IVPOLNQSKLRLDNQWEKLAKTEBILMEALLA	474
Db	465	ENGVAIRERDREDIVGVEPKTPKPHLYNLNEDPLMSECLVYTKDGTITRVEQADARODIV	524
Qy	475	EISGII1-KGFVCPYKSEMPLVNLNSDPLAEKPLAECLVYTKDGTITRVEQADARODIV	532
Db	525	ISGAIKIKPEKHOLFSESSNTSGEVTYKTCPCBSETYVNGRVAHNPOLLESSNRMKXNH	584
Qy	533	LNGSKLILKEHTF-E-NVDN-NTVYNEKAAWYNGVDRKPTRLSGTRILGDFH	587
Db	585	VFRNHPPQAAERE_599	
Qy	588	IFRFNHPEAAERQ_602	
RESULT	2		
ENTRY		A56921 #type complete	
TITLE		Kinesin family protein KIF1a - mouse	
ORGANISM		#formal_name Mus musculus #common_name house mouse	
DATE		02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change	
ACCESSION		13-Aug-1999	
REFERENCE	A56921	Okada, Y.; Yamazaki, H.; Sekine-Aizawa, Y.; Hirokawa, N. Cell (1996) 81:769-780.	
AUTHORS		The neuron-specific kinesin superfamily protein KIF1A is a unique monomeric motor for anterograde axonal transport	
TITLE		synthetic vesicle precursors for retrograde transport	
		#cross_references MUD:95292344	
ACCESSION	A56921	#accession preliminary; translated from GB/EMBL/DBJ	
#MOLECULE-TYPE	MINA	#molecule-weight 1100000	
#residues	1-1656	#label RES	
#cross-references	DB/9911	NCID:9976234; PMID:BA060221;1; PID:997622	
CLASSIFICATION		#superfamily kinesin-related protein unc-104; kinesin motor domain homology; pleckstrin repeat homology P-loop	
KEYWORD		#domain kinesin motor domain homology #label KMTN	
FEATURE		#region nucleotide-binding motif A (P-loop)	
FEATURE	6-360	#length 1165 #molecular_weight 1100000	
FEATURE	97-104	#checksum 7412	
SUMMARY		Query Match Score 2176; DB 2; Length 1695;	
		Best Local Similarity 54.0%; Pred. No. 0.00e+00;	
		Matches 336; Conservative 133; Mismatches 121; Indels 31; Gaps 1;	
Db	1	MAGAS-VEKAVRVPENPESREMSEDSKCI1CIONSTTIVP-----K-Q-P-K--ETPK 48	
Qy	1	MSSGGNIKVVRVPFAREIDRGANCIWMEGNOTILTPPAEEERKRSKTCIMQPK 60	
Db	49	SSPSWTSIDNTAASQYDRLGEBMLOHAFFEYNYCITAYCQTCGKSTMM 108	
Qy	61	APAFRSWSDK MAPFARQEDLFQD1GPILDNAFKYNNCITAYCQTCGKSTMM 119	
Db	109	GKEDQDGIIIPOLCQEDLSRNDTND-NMSVSYEVSMEYTCERVLNPKNGRL 167	
Qy	120	G-YGEGH-GYPRICQDMERRNIEQDKNUFCTVEVSLEYINNVRNLLNPSTKGNL 177	

ACCESSIONS
REFERENCE
#authors Burns Jr., J. M.; Shreffler, W.G.; Benson, D.R.; Ghaliib, H.W.; Badaro, R.; Reed, S.G.
Proc. Natl. Acad. Sci. U.S.A. (1993) 90:775-779
Molecular characterization of a kinesin-related antigen of Leishmania chagasi that detects specific antibody in African and American visceral leishmaniasis.

#cross-references MUID:93133867
#accession A47334
#molecule-type DNA
#residues 1-958 #label BUR
#cross-references GI:107879; NID:9308884; PID:AAA29254; 1; PID:9308885
#experimental_source MI:OMIM/BR:822BA:2.C1
#note sequence extracted from NCBI backbone (NCBIN:122864, NCBI:122865)

CLASSIFICATION #superfamily unassigned kinesin-related proteins; kinesin motor domain homology

KEYWORDS ATP; P-loop

FEATURE #domain kinesin motor domain homology #label KNOT
#domain nucleotide-binding motif A (P-loop)

FEATURE #domain nucleotide-binding motif A (P-loop)

KEYWORDS ATP; P-loop

SUMMARY #region nucleotide-binding motif A (P-loop)
#length 955 #checksum 7462

Query Match 17.58; Score 953; DB 2; Length 955;
Best Local Similarity 43.5%; pred. No. 1.46e-12; Indels 29; Gaps 18;
Matches 177; Conservative 73; Misnatches 99; Indels 14; Gaps 9;

Db 13 VKVSVTRVPLRERENNAPGKTVYAKKAAAATVYKVLGGSNNSGRAESMGKTTARVAQD 72
Best Local Similarity 43.5%; pred. No. 1.46e-12; Indels 29; Gaps 18;
Matches 177; Conservative 73; Misnatches 99; Indels 14; Gaps 9;

Qy 7 IKVYVTRPENRAEID-R-GAKKIVR-L-TPPPGAAEKKKSGK-G-TIMDGPKA 61

Db 73 FDFDVFVSPVTPACGATPATADHFRTIGPLVQHDFPNSCLEAYGOTSGKTYM 132
Qy 62 FAFDGSYNSFSDK-NA-DNY-ARBDLFDQLGPLDNaFKGWNNCIPAYQTSGGSYSK 118

Db 133 MGADYSAUSLGSQEGNNTVTRICLEFARKASAYAQHSRATVLFYVTEYNNERVDSL-NP- 192
Qy 119 MG----Y-GKEHGVPIRICODMERNILQNDKNUCTEVYSTEYNNERVDSL-NP- 170

Db 193 KGVKGGEVYDVYDREPSPGVELEG-QLVVEGSLDDVVLIEITGVYRHTASTMDR 251
Qy 171 -STKG---NL--KVRPSTGPVDFEVLAVL-VRSQEENLDMGKNTVATNNEET 223

Db 252 SRSRSHAIMLLDRERMTKSCBETRTAKSSRNUYDLAGSERVQSYEQQPKET 311
Qy 224 SRSRSHAVTLLTUKW---HDBETKMDMDEYAKTAKSLSRATSTGATRKEGA 279

Db 312 HINLNLTLTGLGVTDYDLMATKGAQAKQSYVAFRUSKLTFLKLSLGNSKTMATVSP 371
Qy 280 EINRSLSTLGRVIALADMSS-GKQRKNDLVYPROSVLWILKLSLGNSNTMIAISP 338

Db 372 SALNVEETLSLRYASRASDVKVAYNNDPAPTRTELEFOMEDMR 418
Qy 339 ADINFEETLSLRYASRASDVKVAYNNDPAPTRTELEFOMEDMR 385

RESULT 11
ENTRY A57107
ORGANISM DATE 03-Nov-1995 #sequence_revision 03-Nov-1995 #text_change
22-Jun-1999
ACCESSIONS
REFERENCE A57107
#authors Yamazaki, H.; Nakata, T.; Okada, Y.; Hirokawa, N.
#journal J. Cell Biol. (1995) 130:1387-1399
#title KIF1A/B: a heterodimeric kinesin superfamily protein that works as a microtubule plus end-directed motor for membrane organelle transport.
#cross-references MUID:96032268
#accession A57107

ACCESSIONS
REFERENCE S38983
#molecule-type mRNA
#residues 1-747 #label YAM
#cross-references GBID26077; NID:91060922; PID:BA005070-1;
PID:G1005611; PID:q1060923
COMPLEX
#experimental_source brain heterodimer with KIF3A (PIR:BA4259); the KIF3A/3B heterodimer associates with a kinesin superfamily-associated protein (KAPS). (PIR:J5C6161 in testis) to form a heterotrimer
FUNCTION
#description KIF3 complex is a motor protein that provides anterograde fast axonal transport for an unknown cargo
#status nucleic acid sequence not shown
#molecule-type mRNA
#cross-references 1-747 #label YAM
#experimental_source brain heterodimer with KIF3A (PIR:BA4259); the KIF3A/3B heterodimer associates with a kinesin superfamily-associated protein (KAPS). (PIR:J5C6161 in testis) to form a heterotrimer
CLASSIFICATION
#status predicted #label HGL
#domain head globular #status predicted #label HGL
#domain kinesin motor domain homology #label KNOT
#domain homology
#ATP: coiled-coil; heterotrimer; microtubule binding; P-loop
FEATURE
#status predicted #label HGL
#region nucleotide-binding motif A (P-loop)
#domain helical rod #status predicted #label ROD
#domain tail globular #status predicted #label TGL
#binding_site ATP (lys) #status Predicted
#length 747 #molecular_weight 85288 #checksum 7951
SUMMARY
Query Match 17.4%; Score 942; DB 1; Length 747;
Best Local Similarity 46.7%; pred. No. 1.53e-10;
Matches 163; Conservative 73; Misnatches 99; Indels 14; Gaps 9;
Db 37 KLGQYVKNPKGTSHMPKPTFEDAVDWNNAKOFELYDETFPLVDYLOGFNGTIPAYG 96
Qy 50 KSGRTIMDQGPKAFADS-TWSFDKAPNAYRQEDFDQLGVPDLDNFAFGYNMCIPAYG 108
Db 97 QNGQTYYTMGVRGDKPGRVTPNSPDHPTISQHQL---VRASTLEYQDEIR 153
Qy 109 QRGSKSXTSMG-Y-GK-E-HQVTPRICOQDFRINELQNDKLTQTVTVESTLEYNRRV 165
Db 154 DELSKDQTKRLEKPLDGTGVYKDLSSFTETKSYKELEHVMGNQNSVGTANNEH 213
Qy 166 DLLNFSTKGNLKVREHSTGPKYDPLAKVLYPSQEIENLDEGKNTVATDPAETSS 225
Db 214 RSHAFVFTT-ECSEVGLDGENHITRYKGKLNVDLACSERQANTGAGGERLAEAKTINSL 272
Qy 226 RSHAFVFTTQKWHDBETKMDTVEKAKLSDVLAGSERATATGATRKEGEIR 285
Db 273 SALGNVYISALYD--GK--5TH-TPYRDSKTLPLQDLSFGNAKTVMVANGPASYVNE 326
Qy 286 SRSRSHAVTLLTUKW---HDBETKMDMDEYAKTAKSLSRATSTGATRKEGA 279
Qy 327 TUTTURYANRAKKNKPNRNEPDKALLREOJELAKACLEKRSIG 375
Qy 346 TLSTLRYADSAKRKHNAYVNEDENARMIRELKEELAQLRSLQLSGGG 394
RESULT 12
ENTRY S38983
TITLE #type fragment
#cross-references S38983; S72552
#molecule-type mRNA
#cross-references S38982
#organism #formal_name Strongylocentrotus purpuratus #common_name purple urchin
#cross-references S38981
#accession S38983
#status nucleic acid sequence not shown
#molecule-type mRNA

RESULT	15
ENTRY	T11750 - "type complete
TITLE	kinins-like protein 38B - fruit fly (Drosophila melanogaster)
ORGANISM	<i>Drosophila melanogaster</i>

Search completed: Mon Aug 21 15:40:03 2000

search completed: Mon Aug 21 15:40:03 2000

##residues 1-294 ##label COL1
 ##cross-references GB:000936 FlyBase:K1P68D; KLP5
 ##molecule-type protein FlyBase:FBgn0004381
 CLASSIFICATION #residues 247-264 ##label COL2
 #superfamily kinesin-related protein KIF3; kinesin motor
 KEYWORDS domain homology
 FEATURE P-loop
 1-279 #domain kinesin motor domain homology (fragment) #label
 KIF3
 29-36 #region nucleotide-binding motif A (P-loop)
 SUMMARY #region nucleotide-binding motif A (P-loop)
 #length 294 #checksum 4908
 Query Match 16.6% Score 900; DB 2; Length 294;
 Best Local Similarity 16.6%; Pred. No. 7, 69-133;
 Matches 148; Conservative 66; Mismatches 77; Indels 13; Gaps 8;
 Db 1 RQIDYDFTPSLVEYLQSFNITFAYCQTCGTTMGEVRSNPPLRCVTPNSPEHIF 60
 Qy 80 RQELDFQDGLYPDIDAFKQYNCIFAGQGSGRSYSMAGY-GK-E-HEVIFRICQDF 136
 Db 61 THIARTSQQL--WRSASLTYQEEBLRDLAKDQKQRDLKERPDTCWYKWDLSSEFT 117
 Qy 137 RRIINELQDKNLCTCDEVSTLEIYNEVRDILNPSTGNKLVRKHPSTGPYEDLAKLV 196
 Db 118 KSVTEIHEWVAVGNNRGSSTMMHESRSRSRSHAIIITIICSELGIDGENHII-RVKGKLN 176
 Qy 137 RSFQEINLDAEDEGKARTVAAITMNETRSRSRSHAIIITIICSELGIDGENHII-RVKGKLN 256
 Db 177 VDLGASRERAKTATSDRKEATKINLISLAGNIVSALWD-GK-SSH-IPYRDSL 230
 Qy 257 VDLGASRERAKTATSDRKEATKINLISLAGNIVSALWD-GK-SSH-IPYRDSL 316
 Db 231 TRLIQDLSGGNATVWAVNGPASYNEDETITLRYANRANKNPKINEDKDALRE 290
 Qy 317 TWLKLDSGSNSMTAIAALSPADINETSTLRYADSAKRNHAWNEDPNARMIRE 376
 Db 291 FQE 294
 Qy 377 LKE 380

RESULT 13 A55236 #type complete
 ENTRY kinesin-related protein K1P68D - fruit fly (Drosophila
 TITLE melano-raster)
 ATTENATE_NAMES Kinesin-like protein 5; KLP5
 ORGANISM #formal_name Drosophila melanogaster
 DATE 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change
 ACCESSIONES A55236; FA1238
 REFERENCE #authors Pesavento, P. A.; Stewart, R. J.; Goldstein, L. S. B.
 #title Characterization of the K1P68D kinesin-like protein in
 Drosophila: possible roles in axonal transport.
 #cross-references MUID:9505096
 #accession A55236
 #molecule-type mRNA
 #residues 1-704 ##label PES
 #cross-references GB:015794; NID:9595912; PID:9565090
 REFERENCE A41298
 #authors Stewart, R. J.; Pesavento, P. A.; Goldstein, D. N.; Goldstein, L. S. B.
 #title Identification and partial characterization of six members of
 the kinesin superfamily in Drosophila.
 #cross-references MUID:92920074
 #accession E41298
 #molecule-type DNA
 #residues 'TC'222-337 'VRGQV' ##label SITE
 #cross-references GB:M74431; NID:9157791; PID:9157792

GENETICS #gene FlyBase:K1P68D; KLP5
 FUNCTION ##cross-references FlyBase:FBgn0004381
 #description may be part of a motor protein that provides anterograde fast axonal transport
 CLASSIFICATION #superfamily kinesin-related protein KIF3; kinesin motor
 KEYWORDS domain homology
 FEATURE ATP; coiled coil; microtubule binding; P-loop
 1-349 #domain head globular #status predicted #label KIF3
 20-350 #domain kinesin motor domain homology #label KIF3
 105-113 #region nucleotide-binding motif A (P-loop)
 350-580 #domain helical rod #status predicted #label ROD
 581-784 #domain tail globular #status predicted #label TGL
 SUMMARY #length 744 #molecular_weight 88193 #checksum 3313
 Query Match 16.5% Score 897; DB 1; Length 784;
 Best Local Similarity 46.5%; Pred. No. 2, 73e-122; Indels 20; Gaps 14;
 Matches 157; Conservative 83; Mismatches 72; Indels 20; Gaps 14;
 Db 63 QRKVFTTDAVADASATTTLYHEVPLVPLSVLEGPNCIAYGOTNGKTFMEGVRN 122
 Qy 65 DRSYSPFDKNPAPYARQEDLFQDGLYPLDNEAFKQYNNCICAYGOTGSKSY-SMAGY-GK 123
 Db 123 DELNGLDFRIFQWILHIN-RTE-NGQFLDVSPELEYMELDILKPKNSK-HLEVRER 178
 Qy 124 EH- GQVBRICQDMERINELQDKKLTUTVEVSYLEIYNEVRDILNPSTGKNLVYRH 181
 Db 179 -GSGVYENLHAINCSVEDMVKMVGDKRNTGPTMMHSSSHSAIFMKI-EM-CD 235
 Qy 182 PATEGVYDALKVYRFQIENIMADEGRKATVATANNTTSRSRHAIVTLLTQWHD 241
 Db 236 TET- -NTIKVQKLNIDLTLGASEROKTGAASRLEKAESKINLASSIGNVSAIAS-SS- 291
 Qy 242 EETRKMDTEKVAISLVLVNLGASERATSTGTGARLGEALINRSLSITGRVIALADMSSG 301
 Db 292 -P--H-VPTDSDKLTLQDLSGGNSKTMIAITANGPSVNYNNEATLRYGRSPAKTS 346
 Qy 302 RQKRLQVLPYDSDYLTLWLDSDGGNSMAMIAATSPADINFEETLSTLRYADSAKRN 361
 Db 347 QPKNEDFODAKLKEYQETEIRL-KL- 372
 Qy 362 HAVVNEDPNAMIRELLEAQRSKL 388

RESULT 14 A53939 #type complete
 ENTRY kinesin homolog KHP1 - Chlamydomonas reinhardtii
 ORGANISM #formal_name Chlamydomonas reinhardtii
 DATE 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change
 ACCESSIONES A53939
 REFERENCE #authors Walther, Z.; Vashishtha, M.; Hall, J. L.
 #title The Chlamydomonas FLA0 gene encodes a novel
 kinesin homologous protein.
 #cross-references MUID:94299638
 #accession A53939
 #status preliminary
 #molecule-type mRNA
 #residues 1-784 #label WAL
 #cross-references EMBL:L33697; NID:9497696; PID:AAA21738-1;
 #note authors translated the codon AAC for residue 753 as Asp
 GENETICS #gene FLA0
 CLASSIFICATION #superfamily unassigned kinesin-related proteins: kinesin
 #KEYWORDS motor domain homology
 #FEATURE ATP; coiled coil; heptad repeat; P-loop